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Title of Invention:			•
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1 (bases 1 to 1755)

Schmidt, E.D., Guzzo, F., Toonen, M.A. and de Vries, S.C.

A leucine-rich repeat containing receptor-like kinase marks somatic plant cells competent to form embryos
Development 124 (10), 2049-2062 (1997)

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U93048
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Schmidt,E.D.L., Guzzo,F., Toonen,M.A.J. and de Vries,S.C.

Direct Submission
Submitted (12-MAR-1997) Molecular Biology, Agricultural University
of Wageningen, Dreyenlaan 3, Wageningen 5703 HA, The Netherlands
Location/Qualifiers
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Daucus carota somatic
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                     GGGCTACATAGCTCCCGAGTACCTCTCGACTGGAAAGTCATCAGAGAAGACCGATGTCTT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
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                                                                                                                                                                                                                                                                                                                                                                            2617
                                                                                                                                                                                                                                                                                                                                                                                                                       2557
                                                                                                                                                   2901 TAGTTTACATTATAGGAAACAGAAGATGAAATCTTTGCTTCTCTGTCAATCCTTTTTCTC
                                                                                                                                                                       4658 attaattcccgtaattaattttatgactgtaaaaattggtgttaatttcaccagttgcga 4717
4884 tgccaggttagtcctgtaaatagata--
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                                                                                                                                                                                                                                                                                                                              attaggaaagcttacaaggctaagattcttgtatgactacaaat------c
                                                                                                                                                                                                            tocaccacctccgttcatcccaccatcaacagtacagcctccaggtgatttagtttttat 4657
                                                                                                                                                                                                                                                                                                    gaaagctatgataatattttttttctccttcatatattatcactttcgcagttttggcaa 4537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACAAACTTAGTGAGTTTGGATCTTTACTTAAACAGCTTCTCCGGTCCTATTCCGGAATC 2316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gacaaatttggtgagcttggacctatacatgaatagcttctctggacctataccggacac 4093
                                                                                                                                                                                                                                         TAACTTAGACCTATGTGGACCTGTTACAAGTCACCCATGTCCTGGATCTCCCCCGTTTTC
                                                                                                                                                                                                                                                      taatttgaatttatgtggacctgtaactgggaggccctgccctggatctcccccattttc 4597
                                                                                                                                                                                                                                                                                     TGAACTTATTCTGAAACTTTCATTTC------CTTGTGCAGTTTTGCTAA 2780
                                                                                                                                                                                                                                                                                                                                                                          AGATCTATCAAATAACAGACTCTCTGGTTCAGTTCCTGACAATGGCTCCTTCTCACTCTT 2676
                                                                                                                                                                                                                                                                                                                                                                                       ggatttatcaaacaatcggctatcaggaccagtaccggataatggctcattttctttgtt 4417
                                                                                                                                                                                                                                                                                                                                                                                                                    TACAGTCTTTGTTTAATCTTAGGTTTTGTTCCAATTTTTGACTCTTTGCTGAAAATTTTA 2436
                     CTCCTGCAATAGCCTTTGCTTGGTGGCGACGAAGAAAGCCACTAGATATTTTCTTCGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTGGGAAAGCTTTCAAAGCTGAGATTTCTGTGAGTATACATATGCTTTTACCGGCTCAGT 2376
                                 cacctgcaatggcatttgcatggtggcggagaagaaaaccgcgagaacatttctttgatg
                                                                                                                                                                                               TCCTCCACCACCTTTATTCAACCTCCCCCAGTTTCCACCCCGAGTAAGCCTCCTCTTT
                                                                                                                          ------aagtattttccttctttcttattattatgaaggacaaa 4763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 387.4; DB 5;
Pred. NO. 4.8e-57;
0; Mismatches 506;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                          4883
                                                                                    4823
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                     3140
                                                               3080
                                                                                                                                                     2960
                                                                                                                                                                                                2900
 4910
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REFERENCE AUTHORS	TITLE JOURNAL	REFERENCE AUTHORS	TITLE		REFERENCE AUTHORS		SOURCE	ACCESSION VERSION	LOCUS DEFINITION	RESULT F23M19/c	Db 3741	Оу 5398	Db 3681	Qу 5338	Db 3621	Qy 5278	Db 3561	Qy 5218	350	Qу 5158	Db 3441	Оу 5098	338	ري ري	ω	Qy 4984	Db 3261	Qy 4924	w	Ov 4910	Db 3141
,	Direct Submission Submitted (01-MAY-1999)	Theologis,	Walker,M., Davis,R.W., Ecker,J.R., Federspiel,N.A. Arabidopsis thallana chromosome 1 BAC F23M19 seque	Lee, J., Liu, A., Li, J., Kremenetskala, I., Luros, J., Gonzalez, A., Altafi, H., Araujo, R., Chao, Q., Conn, L., Conway, A.B., Dunn, P., Hansen, N., Hulzar, L., Kim, C., Palm, C., Rowley, D., Shinn, P.,	Aralidopsis. 1 (bases 1 to 88401) Vysotskala, V.S., Schwartz, J.R., Yu,G., Toriumi, M.,	Eukaryota; Viride euphyllophytes; eudicots; Rosida	nie. thale cress. A Prabidonsis thaliana	ACOO7454 ACO7454.3 GI:5091613			G 3741	g 5398 .	TCTCAATTACTTTGACGTGAAGTGTTTTTCATGTTTTCCTTTATGGGTTCATAATTGTT 3740	taaaaatgaaatataactccctacactatgttaaggtgttataat	TGGAAGTGTTGCTTCGTGTCTCAGAGGTAAAAACTAAACAATTAAACATCTTGTGCTCTC 3680	tggaagtgttgcgtcatgtttaagaggtatctcagttacaattaccataacttgccagaa 5337		tctacgtggtttctgcatgacacctaccgagcggcttcttgtatatccatacatggctaa 5277		tgcagtttcaaacagaagtggaaatgattag		taaaaggct		ttaqtaccatccttqqaaqaqqtqqatttqqtaaqqtqtataaqqqacqcct 50		agtgcaccttggtcaactgaagaggttttctctgcgagaattgcaagtcgcaacggatac 5043	CAAACTCTTTTGAGTAAAATCTCGATTGCAAAATCTCTATGCAGCCGAAGAAGATCCAGA 3320	tactgtctgtggactttgttttcactgtcattagttaacttcagctgaagaggacccaga 4983	GGAACAACTGTTAATGAAAATCAATACATAAGTCATTGTTTTTAAGTTA 3		

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REFERENCE
AUTHORS
TITLE
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
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On J
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Direct Submission
Submitted (17-JUN-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jun
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Jun 17, 1999 this sequence version
sequence of BAC F23M19 from Arabic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFHFLIGALLEYERCRYULIYNDESPLYHOVSRQILHRYVATPHLASPHIQTCH WHHGLIPVETTYRRQLEYLTSOGGTIALDHLTWSDVLJOSGLHNKSEITGREDTTPIAVVIR GLISDSSAYLKHLAYDTAKTGMNVVISNHRGLGGVSVTSDCFYNAGWTDDIRVULDY LOHKYPRAPLFALGTSIGANVLWKYLGESGEKTFLRGAYAICSPWDLLIGDREICRTL KOKLYKALTIGLOGYAQLHEPOPLRANWEGIKKSHSINDDHHAYCLVGKFETVDTYTRKSSSTOYVGNVAVPLLCISALDDPLCTKEAIPWDEGRANKNIVLATTNHGGHLAFFEGLIGSSLWWYBAINEFLGVLSCSFYNHIQKIVDKRSGSGKQEPSINGGFYLNIAE DGLVAAVKYEQDOTKTTLKORGREFEEDVTKKSFKELCRQTKQSVWWLGYIGMVTSFP CGUDLement (5693. .6732)
99ene***TEXMAP. 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref-"taxon:3702"
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\.1"
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Arabidopsis thaliana chromosome 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression Center,
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/note="Contains two PF|00560 leucine-rich repeat domains."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Contains similarity to gi|47
from Zea mays, is a member of the p
glycoprotein family and contains a
protein kinase domain."
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24002. .24145,24225. .24309,24401. .24491,24571. .24735,
24842. .24955,25045. .2517,25210. .25348,25453. .25865,
25953. .26140,26231. .26279)
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VPQIKAEMEKTLOMUVPATRITKAHIGFGWYGEMASSE SANQRPAGQTILRIDTLH
HADKEKTEAVILDLVVWLHHLVTQVRATTGYGLRSPVKSF SANQRKTIQLSGSSHNP
SMGLPLLTTEDQEMLRDVSKRKKTPGISKSQEFETVAKARLCKHRLSKSSSHSPMMG
                                                                                                                                             /evidence-not_experimental
/protein_id="AAD39606.1"
/protein_id="AAD39606.1"
/db_xref="Gi:5091618"
/translation="MINYRHIVECLCYMVVVDSRLTEYLAAIEQUDFIVKIVLFIVGR
/translation="MINYRHIVECLIVGISIISJENLIGTSEHRADLTSLRVIDLS
HNRLKCTIPFEITKLKNLTIUDVSYNQLHGEVFRVRGIVLITERNEVNIESTCLIVFSF
TRNKNKPTVLYLLIGIIVGLVVAGGASFGFYLYRIRKQPKRLQEPNEAVTLTQQQSSD
TRNKNKPTVLYLLIGIIVGLVVAGGASFGFYLYRIRKQPKRLQEPNEAVTLTQQQSSD
ESLYSDESYVISLQVKRVLRRESWVSKGPLLLTRQLKTNQNFHLFYM"
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/gene="F23M19.5"
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/gene="Similar to gb|AF082176 auxin response factor 9
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the PF|00954 S-locus
ins a PF|00069 Eukaryotic
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.40937,41137. .41393,41705. .42256)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gttcctttggttaattatttcacatattagtgcttactactttgttgtggccctttgttt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACCGTGATGTGAAAGCTGCTAATATTCTGTTGGACGAGGAATTTGAGGCGGTGGTAGGT
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tcttttaggttaaaagccttttgaaagagaaaaagttggagatgctggtcgatcctgacc
                                                                                                                                           ttatttcctgcctgtatttgattcttagtcatgttatgcatattgacctgctttgcaatg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGACTATTGGACACATTGCTCCTGAGTATCTCTCAACTGGAAAATCTTCAGAGAAAACT 72571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATTTCGGGTTAGCTAGACTTATGGACTATAAAGATACTCATGTCACAACGGCTGTGCGT
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/db_xref="G1:5091619"
/db_xref="G1:5091619"
/protein_id="F23M19.7"
/protein_id="F23M19.8"
/protein_
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Saccharomyces cerevisiae genome gb|D50617."
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45156. .45311,45523. .45649,45915. .46249,46361. .47119,
47284. .47637,47725. .47869,48023. .48613,48703. .48736,
48815. .48860))
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/protein_id="AAD39608.1"
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/note="Contains similarity to
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Pred. No. 1.5e-56;
0; Mismatches 258;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGAGTTGTCTGGTCCAAGATAAACGACATTGTAATTTGCCTAACAGAAA 72048
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                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (02-NOV-1999) Plant
Submitted (02-NOV-1999) Plant
                                                                                                                                                                                                                                                       Submitted (10-DEC-1999) Plant Gene Expression Center, 800 Street, Albany, CA 94710, USA On Dec 10, 1999 this sequence version replaced gi:6175131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu,S.X., Lee,J.M., Śakano,H., Yu,G., Jhaveri,A., Lenz,C., Toriuni,M., Chin,C., Chiou,J., Choi.F., Gonzalez,A., Howng,B., Koo,T., Li,J., Liu,A., Pham,P., Vaysberg,M., Altafi,H., Brooks,S., Buehler,E., Chao,Q., Conn,L., Conway,A.B., Hansen,N., Johnson-Hopson,C., Khan,S., Kim,C., Lam,B., Nguyen,M., Palm,C., Shinn,P., Tambunga,G., Davis,R.W., Ecker,J.R., Federspiel,N.A. and
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Direct Submission
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Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosome 4 can k viewed at: http://websyr.mips.blochem.mpg.de/proj/thai/.
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Bevan, M., Rose, M., Hempel, S., Entian, K.-D.,
Mewes, H.W., Mannhaupt, G., Mayer, K.F.X. and $
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complement(join(2377. .2571,2755. .2837,3032. .3098, 3180. .3230,3461. .3574,3668. .3724,3815. .3928))
/note-"similarity to Caenorhabditis elegans cosmid, gene T16G1.11, prD:e1349366; contains EST gb:T20620, N65143, T45799, H36819, R65238, N37318"
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gnyhhundrsyassnstywherleehtsavkalmcepqanilatgggggdrikfw
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signature [VLATALDHTYYIMDA] [TGGGGGDRTIKFWNT]
[VASAAGDETLRFWNV]"
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TYXLWDASTGSTSELVTIDEEKGPVTSINWAPDGRHVAVGLNNSEVQLUPDASNOLLA
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SGQQLASGGNDNVVHIWDRSVASSNSTTQWLHRLEEHTSAVKALAWCPFQANLLATGG
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9139...9417,9803...9901))
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pkrhpupdvettpnqqlvisptyvdveleblididldbidkilnpllvashtgybege
pkrhpupdvettpnqqlvisptyvxsbekyplsgfkkmrrelsnnkldqkaagsnkka
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/gene="F17M5.40"

/gene=ht(join(10668. .10967,11056. .11159,11587. .12457,

12511. .12621))
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/gene="F17M5.50"
12884. .14176
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/note="strong similarity to Arabidopsis thaliana
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AACCCACC 50041
                                                                                                                                                                                     ttcgccaatggagcggcctaagatgtcagaggtagtccgaatgcttgaaggtgatggcct
                                                                                                                                                                                                                                             TAATTACAAAGACGAAGAAGTGGAGCAGCTAATCCAAGTGGCTTTACTCTGCACTCAGAG
                                                                                                                                                                                                                                                                     caattacattgacacagaagttgagcagcttattcaagtagcattactctgtacccaggg
                                                                                                                                                                                                                                                                                                                             GGTGAAAGGGTTGTTAAAAGAGAAAATTGGAAGCACTAGTAGATGTTGATCTTCAGGG 50229
                                                                                                                                                                                                                                                                                                                                                ggttaaaagccttttgaaagagaaaaagttggagatgctggtcgatcctgacctgcagaa
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                                                                                                     tccacatc 6586
                                                                               AGCTGAGAGATGGGAAGAGTGGCAAAAGGAGGAAATGTTCAGACAAGATTTCAACTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ACATATATGAGTTTCCCACTT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLRFIDYCYTEKHICWHEIYDFDSDLWTTLDVTPHWYILSNWSCVQGVSLKGNTYWCA
REENSDGYNHIICFDFTRERFGPLLFLPVNVIDNEYEYVTSSCVREGKIAALFQHNDS
YPYELEIWITTKIEAEMVSWNKFLRIDIEPNNNIMVFFIYGGFFIDEEKKKVALGFDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFGRKTFNIIGEDGYFREFDRITFNIIEEAGERAGVNCGSYVCSYVPSLVRIKKPAQG
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Pred. No. 2.4e-45;
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nes 204;
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SOURCE
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fftp://www.cbs.dtu.dk/services/NetGene2/), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named affer the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by trNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are numbered from the top to the bottom of the chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (13-DEC-1999) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA On Dec 17, 1999 this sequence version replaced gi:4726109. The sequence and annotation of chromosome 2 were merged from thos of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D., Fujil,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E., Feldblyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M., Keo,H., Moffat,K.S., Cronin,L.A., Shen,M., Yanaken,S.E., Ummyam,L.,
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Arabidopsis thaliana
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20083487
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255 of the
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We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F1523, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance in addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software clone

This work was supported by the National Science Department of Energy and the US Department of Ac Agriculture Foundation

all correspondence to:

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FEATURES
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/gene="At2g13670"
<3349..>5997
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TQEEEDDAVVUSTPALRSESFRAFKIEVTGSGLSEGYDARLSLKGRNGGGULVLELS
LEVLAANSDVESGLIAEEKKCSSSSSSLGLKNTCRIEVCDVENLGVFRETVELMFEES
NVIIKKPMTMGYYRAIDVLEVVAGIKFSRAVLSCTKTLEAVPWFEDEEEKLRRLIGIF
SFDDAVSEILLARENSBFTENLQDSLSKKLVMSITSCSDVNPRNELKSLVKGLLCKSI
VYEKBQPEINKEDIYRAGKCCVDSLAKLLFEEGSSSSKKEKPLIESISREVENINHL
LEIMIDREIAEEFVEIMGKGRRLVEMHERVSDWYRYEVSRVTGALFIAMGKRRVGCGG
EARAGLVEAMFKPMLVDFGWLORCKGLDMREVEEGMGQTLLTLPVKEQYQVEMEMFR
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                                                                                                                                                                                                                                                                                                                                                         complement (14929. .>17114)

gene="At2g13690"

/note="F13111.4; predicted by genscan and genefinder"

complement(join(14929. .15843,16401. .17114))

/gene="At2g13690"

/note="Apythetical protein"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="At2413670"
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/gene-"At2g13660"
/note-"F13J11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KASRYKKTDGREVESFYQQYYEHYVRALDQGDQADRAQLGKAYQTAGVLFEYLMAVN
KSEKYBAVAFEI IAAARDVQEKNEI YAFYNILFLDSAGASQSYMQLEEYKAAVAALGN
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WGEAANIRFMPECLCYIFHNMAYELHGLLAGNVSIVTGENIKFSYGGDDEAFLRKVIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(517. .842,907. .1114))
/gene="At2g13660"
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ETGIKTGNLKHKPKSSD"
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64516 AAAAAGAAAGCATATTGCTCTGGGATCAGCAAGGGGGCTCGCATATTTACACGATCATTG 64575
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complement(35689...35776)
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33252. 33473)
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Sequence 32 from Patent W
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                    De, V.S., Schmidt, E.D., Van, H.G. and PRODUCTION OF APOMICTIC SEED Patent: WO 9743427-A 20-NOV-1997; CIBA GEIGY AG (CH)
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195. .2072
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Length

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1541 5920 5800 agagegteageeateagaaceteeecetgattggeeaactagggagaggattgeactagg 1721 1661 6100 6040 1361 AGAGAGGCCACCGTCACAACCTCCGCTTGATTGGCCAACGCGGAAGAGAATCGCGCTAGG 1758 6340 6220 6160 1938 1878 6460 1818 6400 1757 6280 Local Sinhes 524; CTCAGCTCGAGGTTTGTCTTACCTACATGATCACTGCGATCCGAAGATCATTCACCGTGA 1480 atcttctaggggcctatctaaattgcatgaccattgtgatcccaagattatccatcgcga 5919 gttagctaggctcatggattacaaggatacccatgttacgactgctgtaaggggtaccat 6039 aattacattgacacagaagttgagcagcttattcaagtagcattactctgtacccagggt 6459 GTGAAAGGATTGTTGAAGGAGAAGAAGCTAGAGATGTTAGTGGATCCAGATCTTCAAACA gttaaaagccttttgaaagagaaaaagttggagatgctggtcgatcctgacctgcagaac tgcctgtatttgattcttagtcatgttatgcatattgacctgctttgcaatgtcttttag 6339 tggttatgggataatgctcctagagctcattactggacagagggcttttgatcttgctcg CGGTCACATCGCTCCAGAATATCTCTCAACCGGAAAATCTTCAGAGAAAACCGACGTTTT 1660 tgggcacatagctcccgagtacctctcgactggaaagtcatcagagagaagaccgatgtctt 6099 GTTGGCAAAGCTTATGGACTATAAAGACACTCACGTGACAACAGCAGTCCGTGGCACCAT 1600 ggttaattatttcacatattagtgcttactactttgttgtggccctttgtttttatttcc GCTAGCTAACGACGACGTCATGTTACTTGACTG-----**AACTACGAGGAGAGAACTGGAACAAGTGATACAAGTGGCGTTGCTATGCACGCAAGGA** Similarity 60.4 24; Conservative 3.7%; Score 250.4; DB 5; Pred. No. 1.5e-33; 0; Mismatches 201; Indels 143; -----G Gaps 1540 5979 1420 5859 6519 1877 6399 1757 1757 6279 1757 1720 6159 1997 6579 1937 ۲

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yasukazu Nakamura, Kazusa DNA Research Institute, Laborato Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan (E-mail: Ynakamu@kazusa.or.jp, Tel:+81-438-52-3935,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakamura, Y.
Structural Analysis of
Unpublished (1998)
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/strain="Columbia"
/db_xref="taxon:3702"
/chromosome="5"
/clone="MON23"
/clone=1b="Mitsui P1"
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                               Direct Submission
Submitted (02-Apr-1999) to the DDBJ/EMBL/G
Yasukazu Nakamura, Kazusa DNA Research In
Gene Structure 2; 1532-3, Yana, Kisarazu,
(E-mail:ynakamu@kazusa.or.jp, Tel:+81-438
Fax:+81-438-52-3934)
                                                                                                                                                          Structural Analysis of Arabidopsis thaliana Unpublished (1999) 2 (bases 1 to 84896)
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
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Unpublished (1997)
2 (bases 1 to 120787)
2 Federspiel, N.A., Davis, R.W., Conway, A.B., Palm, C.J., Conway, A.R., Federspiel, N.A., Davis, R.W., Conway, A.B., Falm, C., Li, Y., Shinn, P., Sun, H., Oji, O., Osborne, B., Shen, Y.K., Toriumi, M., Vyotskaia, V., Yu, G., Theologis, A. and Ecker, J.
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Direct Submission
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Submitted (05-JUN-1997) Blochemistry,
Sequencing and Technology Center, 855
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                                                                                                                                                                                                                                                                      Submitted (02-OCT-1997) Biochemistry, Sequencing and Technology Center, 855
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                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (11-JUL-1997) Biochemistry, Stanford University/DNA Sequencing and Technology Center, 855 California Avenue, Palo CA 94304, USA
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Submitted (09-UUL-1997) Biochemistry, Stanford University/DNA Sequencing and Technology Center, 855 California Avenue, Palo
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Location/Qualifiers
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join(177. 214,632.
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177. .2876
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RGELERLEKLMNKYERGOIQSIDWLDRLMLKSLDTIKEOESTKHGSSHLFVVIDFCSF
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SELTYTEEPEIRSPLTPUNLIKGIVAGESSLFKSALHBLRLTFRTPEEGGSCKLIFKKG
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ERSITSYLQKHEDDEHAPFGITATCLDTFIKSCAGYSVITYIIGIGDRHLDNLLLTDD
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10509. .10653,10780. .10917,10991. .11164,11286.
11815. .11936,121477. .12182,12300. .12395,12475.
12803. .12981,13104. .13313,13414. .13572,13659.
13867. .13963,14069. .14180))
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GLKKVKSAYPLVVAMLDVPEBHREILASQGCVVREIEPVYPDNQVEBAMAYVYLNY
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GYCQCDEKVTWPEDMESPPPLYFNAGMFYFEPSPLTYESLLCTLEITPSPFRAEQD
FLNMEFEKVYKPIPLYYNLYLAMLWRHPENVELEKVKVVHYCAAGSKFWRYTGEBANM
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/gene-"F8A5.2"
complement(join(3171. .3389,3471. .3605,3706. .4029,
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MCDYCJSDREHLKVGSGTVCQEDKHKRVGGTMEVVIVISDLLESTQHCSRSCNGKTEV
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HWYHNQYFTRQKNGFGISLLKKGIKNKLDNLKAKHEGFLLSSHSRKICSFVYPDLARSI
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complement(join(8347. .8443,8539. .8657,8941.
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VWDVSCKTEGLIGGATVLLFNSKMONKSGKOKLRLWGGKEADGSFFTSTPGKVPRHE
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protein gp|D26537|537404"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative ADP-ribolylation factor"
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/protein_id="AAB71966.1"
/db_xref="GI:2462747"
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                                                                                    note="similar to "Mx" GTP-binding
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Db 108599 TGGGACAGCGAGAGGACTAGTTTACCTACACGAGCAATGTGACCCGAAGATTATACACCG
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cattgggcacatagctcccgagtacctctccgactggaaagtcatcagagaagaccgatgt 6096
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                                                                                                                                                          TGGGTTAGCTAAGCTTCTAGACCATAGAGACTCTCATGTCACAACTGCAGTCCGTGGAAC
                                                                                                                                                                                                                     CGATGTGAAAGCAGCTAACATTCTGTTAGATGAGGACCTTCGAAGCAGTTGTTGGTGATTT
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EBARMGELLERTHPVLSLIDEDIYGIPVLAQKIMLIOSSMIARCLPKIVSKINQKLD
TAVLELINKLEMVMASTGEALMALMDIIGSAKISLLRILYGGDE'SEYPDDQNMHCTAKLD
ADMLSQFSDSLQAKPKEVAEFLMDEIKILDECKCVGLPNFIPRSAFLAILSQHVDGIQ
DKPVEFINKINDY IEDVLSSVTAKRSDNFPQIOSSIKBAGRNLISKI KEQSVNRYMEI
VEMERKLTDYGVDFEYNFYGVTSAGAGESFIDAVYKNENIDVE'SYTGFENWKISHIRK
YHAHLLIPAFDMKMRITSYWKIVLRRIVDNLALYLQLSVKSLVNTRFQKEIVAEMVDP
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PLDDTVDRLKHLNVMREGIHLPTIVVVGDQSSGKSSVLESLAGISLPRGQGICTRVPL
VMRLQRSSSPEPEIMLEKUDKVVPTDEBHIAEAIRAATDVIAGSGKGVSDAPLTLHVK
KAGVPDLTMVDLPGITRVPVNGQPENIYEQISGMIMEYIEPQESIILNVLSATVDFTT
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//db_xref="G1:2462738"
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/translation="Mogskmandyzidyeagmsslsivntpieapiyssyndrirplidtyddenslation="Mogskmandyzidyeagmsslsinlprgogictryddymr.corsspepeiwleysbxvprpdeebyaealcaatdyzagtgesysorplilsykknn.corspepeiwleysbxvprpdeebyaealcaatdyzagtgesysorplilsykknn.vpdlinyddegitrydyngopeniyegismimkyiepoesiilnylsatydfticesirmsroydktgertlayvtkadmapeglligkytaddysiglgyicvrnrigeeryeea
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21973. .22091.22335. .22510)
/gene="#985.6"
/note="similar to "Mx" GTP-binding proteins"
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complement(join(26476. .26936,27030. .28070,28540.
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/gene="F8A5.7"
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2 (bases 1 to 134784)

Sun, H., Wohldmann, P., Johnson,
The sequence of A. thallana F.
Unpublished (1999)
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                                                                                                                Actual end is
                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problem such as compressions and repeats; all regions were covered by sequence from more than one subclone
                                                                                                                                                                                                                                                                                                                                                                                                                               MAPPING: Clones were assigned to the YAC map by hybridization by M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted by M. Marra, WashU, to pick the best candidates for sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (17-JUN-1999) Department of Genetics,
University, 4444 Forest Park Avenue, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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                                                                                                                                                                                                                                                                                                                                  neighboring submissions.
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                                                                                                                                                                                                                                                                                                                                              TICE: This sequence may not be the entire insert of this clone.

may be shorter because we only sequence overlapping sections

ce, or longer because we provide a small overlap between
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                                                                                                                start of this clone
at 134784 of F17123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Sequencing Center
Department of Genetics, Washington
St. Louis, MO 63108, USA
e-mail: rwilson@watson.wustl.edu
                               /organism="Arabidopsis
/cultivar="Columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by:
                                                                                                Location/Qualifiers
 /clone="F17123"
/chromosome="IV"
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Missouri 63108,
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                                                                                                                                                                                                                                       gggacgagtggcaaaaagttgaagtcatccatcaagac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCATAAGATCAACCAAATTAACATTTCTCCCGGATGCTGTTGTA-----
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                                                                                                                                                                                                                    GGGCTGCTTCGCATAACCATTCACATTTCTACCATGCC 47229
                                                                                                                                                                                                                                                                                  ATCGTCCTAAAATGTCTGAAGTTGTTTTGATGCTTGAAGGCGATGGATTAGCCGAGAGAT
                                                                                                                                                                                                                                                                                                                                                                               acacagaagttgagcagcttattcaagtagcattactctgtacccagggttcgccaatgg
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                                                              AB005234 89779 bp
Arabidopsis thaliana complete sequence.
AB005234
AB005234.1 GI:2264306
clone:MBK5.
Arabidopsis
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30; Conservative
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Pred. No. 9.5e-24;
0; Mismatches 273;
                                                                                                                genomic
                                  (strain:Columbia) DNA,
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clone: MBK
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                                                                                                                                                                                           55313 CTTGATCATGTAAGATTGACTTCTTTTACATGCTTT 55348
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                                                                                                                                                                                                                                                                                                                                                                    actggaaagtcatcagagaagaccgatgtctttggttatgggataatgctcctagagctc 6127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acccatgttacgactgctgtaaggggtaccattgggcacatagctcccggagtacctctcg 6067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACAATTTTGAGCCAGTTCTTGGAGATTTCGGTTTAGCTAAGCTTGTGGACACATCTCTG 55132
                                                                                                                                                                                                                           ttggattgggtatgtgtcccgggtgttcctttggtt 6223
                                                                                                                                                                                                                                                                    GTTACTGGTCAGCGCGCAATCGATTTTTCACGCTTGGAAGAAGAGGAAAATATTCTCTTG
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complete sequence. AC005170 AE002093 AC005170.2 GI:6598 HTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUL-1997) to the DDBJ/EMBL/GenBank databases. Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935, Fax:+81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sato, S., Kotani, H., Nakamura, Y., Kaneko, T., Asamizu, E., Fuka Miyajima, N. and Tabata, S. Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             physically assigned P1 clones
DNA Res. 4 (3), 215-230 (1997
97471969
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                                                                      AC005170 110211 bp
Arabidopsis thaliana
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Similarity 65.7%;
60; Conservative
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/strain="Columbia"
/db_xref="taxon:3702"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="MBK5"
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16340 c 16159 g 28865
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                                                                         DNA PLN 17-DEC-1999 chromosome II section 135 of 255 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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Pred. No. 1.6e-21;
0; Mismatches 136;
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    repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inn.X., Kaul,S., Rounsley,S.D., Shea,T.F., BeullCH., Rujil,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E., Feldblyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M., Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayam,L., Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H., Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D., Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
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Submitted (13-DEC-1999) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
On Dec 17, 1999 this sequence version replaced gi:3738313.
The sequence and annotation of chromosome 2 were merged from those
of the individual clones on this chromosome after removing
overlaps. For detailed information, please see the TIGR web site
(http://www.tigr.org/tdb/at/at.html).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6523, F5J6, T17A5, and T13L16, the ESSA group for sequencing clons F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satcshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu. Feng Liang, Jeremy Shou, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thale cress.
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                Address all correspondence to: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are numbered from the top to the bottom of the chromosome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis.
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/note="Sequence from
complement(356. .401)
                                                                            complement(1. .2793)
                                                                                                                                                                                        /organism="Arabidopsis
/cultivar="Columbia"
                                                                                                                    /chromosome="2"
                                                                                                                                                    /db_xref="taxon:3702"
                                        clone F27L4"
                                                                                                                                                                                                                                                                                                                                at@tigr.org.
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complement(join(1549. .2058,2731.
/gene="At2923810"
complement(1549. .3012)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / LPC_ramily="(TAAA)n" complement(3570. 364
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GKRYENGKKWNKIRSCLYESKYCSKLEAKFYNYPYNSFYKEHLTALGSGCCKPSDECG
FEYYNPTTWTKNTTGTHENBDCQTWDNAKEKLCFDCQSCKAGLLDNYKSAWKKYAIVN
IVFLVFLIIVYSYGCCAFRNNKRDDSYSRTYGYKP"
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/note="F77"
                                                                                                                                                                         /translation="MSNNELLEIEPMYLQFPFELKKQMSCSLYLTNKTDNNVAFKVKT
TNRNNYCVRNYGLILFKSTCKVLYTMQAQKEVPSDMQSFEKEMIQSYLASPGVTAKE
VTREMFSKESGHVVEETKLRVTYVCSTTTNITSSPRTRRGFIFQCFC"
complement(11332...11371)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MKNVNRVFFCKSLSLVFLVPSFTRSHIRFTYSAAGASSPNRAIH
CMASDSPÖSGDGSVSSPPNVAAVPSSSSSSASSAIDFLSLCTLKKTTPRAGWIRDDV
KDPESIADHWYRMGLMALISSDIFFUNDAKCKKMAATYHDIAEAIVGDITESGGISKEE
KNRRESEALEHMCKLLGGGERAKEIAELWREYEENSSPEAKVVKDFDKVELILQALEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Sequence from clone T29E15"
complement(3567. .3677)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="similar to senescence-associated protein"
/protein_id="AAF18611.1"
/db_xref="G1:6598449"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(6654. .6712)
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8152. .8268,8487. .8557)
/gene="At2g23820"
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complement(join(<20442.
21145. .>21485))
                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="At2g23830"
<9531. .>10396
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join(<6480. .6749,7602.
B152. .8268,8487. .8786)
/gene="At2g23820"
                                                          /rpt_family="
16051..16136
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/note="T29E15.3"
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/db_xref="GI:3738315"
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                    .20537,20617.
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                         ctcccgagtacctctcgactggaaagtcatcagagaagaccgatgtctttggttatggga 6110
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29302. .29885
/gene="At2g23870"
/note="T29E15.7"
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complement(29076. .2910
/rpt_family="POLY_A"
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21145. .21485))
/gene="At2g23840"
/note="unknown protein"
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/gene="At2g23840"
/note="T29E15.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(<31877. .32176,32267. .32407,32498. .32893,
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/gene="At1223880"
complement(<31877. .>36147)
/gene="At223880"
/note="T29E15.8"
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/gene="At2g23850"
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MSRLKFCARIFSSYSFPYKRKKIRDLDNTEKNLDIDEDNDEWDFDGDDDGLETDDHLS
CFRGLVLDISYRPVNVCWKRAICLEYMDKADVLEYYDQTVSSPTGSFYIPAVLRVPH
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/db_xref="GI:3738318"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(<22999. .23070,23189.
/gene="At2g23860"
<22999. .>23554
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/rpt_family="(TA)n"
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/note="unknown protein"
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/db_xref="GI:3738317"
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Sequence 6695 BP; 1844 A; 1182 C; 1243 G; 2422 T;
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Best Local Similarity
Matches 6692; Conserv
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2880 2880	1 agtggctgtagtagaacaccttaagcaagaacttaatcatgaggtttcaaccttttaact 	282	gg dg
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TAAGAAATAGTGAATCAAATTATCGTGTTATTGTGTTTTGTAC 3	TAATAGTGGATGATCATT	3301	망	
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ACCTCCCACTAGCCTTTCGTTGTTTTATTCACAGTTCACACA 3	TATAGGTTTAAGGCTTGC	3181	망	
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	4740 4740	1 tgactgtaaaaattggtgttaatttcaccagttgcgaataaagtattttccttctttct	Qy 468 Db 468	
	4680 4680	1 catcaacagtacagcctccaggtgatttagttttttatattaattcccgtaattaat	Qy 4621 Db 4621	
	4620 4620	1 taactgggaggcctgccctggatctcccccattttctccaccacctccgttcatcccac	Qy 456 Db 456	
	4560 4560	1 totoottoatatattatoaotttogoagttttggcaataatttgaatttatgtggacotg 	Qy 4501 Db 4501	
	4500 4500	1 gtaatatotttaatattatggttottaottotaotgcgaaagotatgataatattttttt	Qy 444 Db 444	_ ^
	4440 4440	1 caggaccagtaccggataatggctcattttctttgtttacacctatcaggtttaatgcta 	Qy 438 Db 438	_ ^
	4380 4380	1 tggatgtttcaattttaatactaaatatgttcatcagggatttatcaaacaatcggctat 	Qy 4321 Db 4321	
	4320 4320	1 aatattacaactottcaagtcotgtaagtattocgacotttocagatagttttgttgttg	Qy 426 Db 426	
	4260 4260	1 ttactggataggcgtctcaacaactagctctctggtccaattccaatgtcactgact	Qy 420 рь 420	
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Production of apomictic seeds - useful in plant breeding
Production of apomictic seeds - useful in plant breeding
Claim 21; Pages 47-51; 123pp; English.

CC The sequence is that encoding SERK, a putative receptor kinase.

CC It may be used as part of a method of producing apomictic seeds

CC comprising: (a) transforming plant material with a nucleotide

CC sequence encoding a protein which in active form in a cell or

CC cell membrane renders the cell embryogenic; (b) regenerating

CC the transformed material into plants or carpel-containing

CC plant parts; and (c) expressing the sequence in the vicinity

CC of the embryo sac. The apomictic seeds and embryos thus produced

CC can be developed into plant progeny. This is useful in plant

CC the case that sexual plant improvement and cultivar development in

CC the case that sexual plants are available as crosses with the

CC apomictic plant. Apomixis provides for true-breeding, seed

CC propagated hybrids and could shorten and simplify the breeding

CC process so that selfing and progeny testing to produce and/or

CC stabilise a desirable gene combination could be eliminated.

CR Apomixis allows plant breeders to develop cultivars with

CC specific stable traits for such characteristics as height,

Sed and forage quality and maturity.

SO Sequence 1814 BP; 530 A; 354 C; 415 G; 515 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Daucus carota SERK graceptor kinase; apor
plant breeding; ss.
Daucus carota.
Key Loca
CDS 94.
                                                                                                                                                                                                                                                                                                                                                                                                                                20-NOV-1997.
13-MAY-1997;
14-MAY-1996;
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De Vries SC, Hecht VFG,
WPI; 98-086529/08.
P-PSDB; W47013.
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RESULT V06585 ID VI AC VI DT 0: DE A:

V06585 standard; DNA; V06585; 03-AUG-1998 (first en Arabidopsis thaliana 9

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tggttatgggataatgctcctagagctcattactggacagagggcttttgatcttgctcg
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                                                                                    TCGCCAATGGAGCGGCCTAAGATGTCAGAGGTAGTCCGAATGCTTGAAGGTGATGGCCTT
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Pred. No. 9.1e
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.1e-108;
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apomixis; apomictic; seeds; production; embryos;

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                                                    Query Match
Best Local Similarity
Matches 903; Conserv
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13-MAY-1997; E02443.
14-MAY-1996; GB-011044.
(NOVS ) NOVARTIS AG.
De Viles SC, Hecht VFG, S
                                                                                                                                                                                                                                                                                            production of apomictic seeds - useful in plant breeding Claim 26; Pages 64-67; 123pp; English. The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing
  2197
                                                                                                               apomictic plant. Apomixis provides for true-breeding, seed propagated hybrids and could shorten and simplify the breeding process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.

Sequence 4081 BP; 1120 A; 770 C; 785 G; 1406 T;
                                                                                                                                                                                                                     plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the
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plant breeding; ds.
Arabidopsis thaliana
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P-PSDB; W47017.
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Pred. No. 4.1e
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                            tactgtctgtggactttgttttcactgtcattagttaacttcagctgaagaggacccaga
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Claim 27; Pages 91-95; 123pp; English.

Claim 27; Pages 91-95; 123pp; English.

If may be used as part of a method of producing apomictic seeds comprising; (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated.

Apomixis allows plant breeders to develop cultivars with
                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis .
Key
CDS
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20-NOV-1997.
13-MAY-1997; F
                                                                                                                                                                                                                                                                                                                                                                                                         receptor kinase; apomixis; plant breeding; ds. Arabidopsis thaliana.
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03-AUG-1998 (first e
Arabidopsis thaliana
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WPI; 98-086529/08.
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         totggtccaagataaacagcatataaaa
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TCTGGTCCAAGGTAAAAAAAAAAAAAA
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2089 BP; 568 A; 419 C; 503 G;
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Matches 214;
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17-JUL-1998; U14841.
13-AUG-1997; US-910386.
(REGC ) UNIV CALIFORNIA.
Hulbert SH, Richter T, Ro
Wang G;
WPI; 99-204431/17.
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This invention describes a method for conferring disease resistance plants. The invention describes the use of novel genes and proteins belonging to the Oryza longistaminata and Oryza sativa receptor kinase-like protein (RRK) Xa21 multigene family. Such genes from cassava, maize and tomato are also described. The genes and proteins be used for enhancing resistance to Xanthomonas in a plant, preferal
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plant disease resistance; c
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Tomato RRK gene clone TRK1
Xa21; RRK; disease resista
tomato receptor kinase 1;
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                     Lycopersicon esculentum WO9622375-A2.
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nase 1; TRK1; transgenic plant; c;
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maize; tomato;
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.2e-15;
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ato; Xanthomonas;
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plant, preferably in
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                                                                                         protection;
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CDNA clones TRKI (T31307) and TRLI (T31308) were isolated from tomato cDNA library by screening with probes generated by PCR amplification of tomato cDNA using primers (T31301-06) based on the rice disease resistance Xa21 gene (T31300). They belong to the RRK family of disease resistance genes. TRKI (tomato receptor kinase 1) is present as 1 or 2 copies in the tomato genome and 1 copy maps to the Short arm of chromosome 1 in the proximity of a resistance gene to Xanthomonas campestris pv. vesicatoria RXI. It encodes an RKK protein (W03186) that is an important component of plant signal transduction pathways leading to affence response. The gene 1s useful for engineering disease resistance in tomato and other plants. Sequence 1554 BP; 477 A; 303 C; 348 G; 426 T;
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Best Local S
Matches 197
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17-JAN-1995; US-373374.
17-JAN-1995; US-475891.
29-SEP-1995; US-004645.
(REGC ) UNIV CALIFORNIA.
Ronald PC, Song W, Szab
WPI; 96-354532/35.
P-PSDB; W03186.
Wang G;
WPI; 99-204431/17.
P-PSDB; W93600.
New RRK polynucleot
                                                     25-FEB-1999.
17-JUL-1998; U14841.
13-AUG-1997; US-910386.
(REGC) UNIV CALIFORNIA.
Hulbert SH, Richter T, Ro
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X23532;
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                                                                                                                                                       Xa21; receptor kinase-like protein;
plant disease resistance; cassava; 
                                                                                                                                                                                    Tomato Xa21 clone TRK1
                                                                                                                            Lycopersicon esculentum. WO9909151-A2.
                                                                                                                                                                                                 17-JUN-1999
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polynucleotides
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Pred. No. 2.3e
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Xanthomonas in
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2.3e-14;
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P-PSDB; W13408.

P-PSDB; W13408 with short stems or altered inflorescence yield plants with short stems or altered inflorescence Claim 1; Pages 6-10; 17pp; Japanese.

The present sequence encodes an Arabidopsis thaliana plant morphogenesis regulatory protein (MRP), which can be used to yield a plant with, e.g. short stems or altered inflorescence. The MRP acts on a plant at a specific site for a specific period, and can therefore be used to regulate extraneous gene expression in a plant. The MRP's cDNA or genomic DNA can be used to transform a plant to increase its MRP expression, and therefore control the
                                                                                                                                                                                                                                                                                                                                                 J09056382-A.
04-MAR-1997.
24-AUG-1995; 216187.
24-AUG-1995; JP-216187.
24-AUG-1995; JP-216187.
(MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
(CHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYU.
WPI: 97-206629/19.
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Arabidopsis thaliana plant morphogenesis regulatory protein cDNA.
Plant; morphogenesis; regulation; short; stem; alteration;
inflorescence; extraneous; gene; expression; transformation;
increase; control; form; length; ds.
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This invention describes a method for conferring disease resistance plants. The invention describes the use of novel genes and proteins belonging to the Oryza longistaminata and Oryza sativa receptor kinase-like protein (RRK) Xa21 multigene family. Such genes from cassava, maize and tomato are also described. The genes and proteins
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/note= "plant morphogenesis regulatory protein"
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control; form; length;
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F 24-AUG-1995; 216187.
F 24-AUG-1995; JF-216187.
R 24-AUG-1995; JF-216187.
A (CHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYUSHO.
NA (CHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYU.
NA WPI; 97-206629/19.
PT DNA encoding plant morphogenesis regulatory protein - useful to present with short stems or altered inflorescence PS Claim 6; Pages 12-15; 17pp; Japanese.
Claim 6; Pages 12-15; 17pp; Japanese.
CC The present sequence encodes an Arabidopsis thaliana plant companies of the present sequence of the present sequence which can be used to morphogenesis regulatory protein (MRP), which can be used to morphogenesis regulatory protein (MRP), which can be used to morphogenesis regulatory protein (MRP), which can be used to morphogenesis regulatory protein (MRP).
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                                                  contraceptive; ss.
Arabidopsis thaliana.
Key Locatt
CDS 97...
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Sequence 9295 BP; 2873 A; 1581 C; 1602 G; 3239 T;
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Arabidopsis steroid receptor Binl DNA.
BINL; steroid receptor; receptor kinase; transgenic plant;
brassinosteroid; disease resistance; crop protection;
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30-DEC-1998.
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55.7%;
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Pred. No. 1.3e-13;
0; Mismatches 163;
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Matches 200
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Chory J, Li J;
WPI; 99-081275/07.
P-PSDB; W97819.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant yield or vegetative biomass and increased seed yield. Expression of Binl may also increase resistance to pesticides. Inhibition of Binl, e.g. using antisense oligonuclectides (AON), is used to render plants male-sterile, and to reduce their stature or yield, e.g. for creating dwarf varieties. Since Binl homologues may be involved in regulation of the menstrual cycle and uterine function, Binl, antibodies and AON may be seful as contraceptives, for improving success of in vitro fertilisation and to prevent premature labour. Transgenic animals are also provided, and are models for studying steroid-receptor interactions or can be used
                                                                                                                                                                                                                                                                                       6005
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24-JUN-1997; US-881706.
(SALK ) SALK INST BIOLOGICAL STUDIES
X23531 standard;
X23531;
17-JUN-1999 (fin
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plants and for modulating occyte maturation
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                                                                                                                                                                                                                                                                                                                                  gacgaagaatttgaggctgttgtaggtgattttgggttagctaggctcatggattacaag
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4104 BP; 1061 A;
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(first entry)
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                          CDNA; 3045
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Pred. No. 2.9e
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17-JUL-1998, U14841.
13-AUG-1997, US-910386.
(REGC ) UNIV CALLFORNIA.
Hulbert SH, Richter T, Ro
20-NOV-1997. E02443.
13-MAY-1997, E02443.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De Vries SC, Heicht VFG, S
                                                                                                                                                                                                              Arabidopsis
Key
CDS
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This invention describes a method for conferring disease resistance plants. The invention describes the use of novel genes and proteins belonging to the Oryza longistaminata and Oryza sattlya receptor kinase-like protein (RRK) Xa21 multigene family. Such genes from cassava, maize and tomato are also described. The genes and proteins
                                                                                                                                                                                                                                                                                03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST clone.
receptor Kinase; apomixts; apomictic; seeds; produc
plant breeding; leucine-rich repeat; ss.
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Xa21; receptor kinase-like protein; multigene family; RRK; rice;
plant disease resistance; cassava; maize; tomato; Xanthomonas; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2494
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99-204431/17.
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                                                                                                                                                                                                                                                             thaliana
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  Schmidt EDL,
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Pred. No. 4.5e-08;
D; Mismatches 161
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13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
(NOVS) NOVARFIS AG.
(NOVS) NOVARFIS AG.
De Vries SC, Hecht VFG, (WPI; 98-086529/08.
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Key
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The sequence is that of an EST clone showing SERK LRR (leucine-rich repeat) sequences.

Sequence 1106 BP; 331 A; 258 C; 20
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receptor Kinase; apomixis; apomictic; see
plant breeding; leucine-rich repeat; ss.
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20-N0V-1997; E02443.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG:
De Vries SC, Hecht VFG, S
WPI; 98-08639/08.
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13-MAY-1997; E02443.

14-MAY-1996; GB-010044.

(NOVS ) NOVARTIS AG.

De Viles SC, Hecht VFG, S

WPI; 98-086529/08.

P-PSDB; W47022.
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                                                                      Claim 28; Pages 86-88; 123pp; F
The sequence is that of an EST
SERK LRR (Leucine-rich repeat)
Seguence 1063 BP; 313 A;
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1: /cgn2_6/ptodata/

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US-08-477-731F-1
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US-08-233-6251-83
US-08-447-185-3
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US-08-447-185-3
PCT-US93-06251-7
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US-08-680-726A-5
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                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/587,680A
FILING DATE: 17-JAN-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
PRIOR APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION NUMBER: US 60/004,645
FILING DATE: 04-DEC-1995
PRIOR APPLICATION NUMBER: US 08/567,375
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 34,774
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-0589
TELEPAN: (415) 576-0300
TELEPAN: (415) 576-0300
TELEPAN: (415) 576-0300
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CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-8834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pair
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APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IEM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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US-07-991-867B-1
US-09-014-069-14
US-09-018-37-36
US-09-056-075-1
US-09-175-581-12
US-09-175-581-12
US-09-187-889-1
PCT-US96-09193-1
US-07-826-09193-1
US-07-826-011A-3
US-08-105-483-220
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US-08-224-391-90
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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA (partial)
US-08-587-680A-24
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Patent No. 5859338
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Best Local Similarity 60.8
Matches 197; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A
FILING DATE: 06-JUN-1995
CCLASSIFICATION: 800
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                   TELEX: 910 277299 INFORMATION FOR SEQ ID
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APPLICANT: Williams, Robert W.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
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                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: S11'va, ROBIN M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         986 AATGGGAAACTAGGCTAAAAATAGCCATAGAAGCTGCCAAGGGCCTTTCTTATTTGCACC 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Four Embarca
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States ZIP: 94111-4187
                                                        TELEFAX:
                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cccatg---ttacgactgctgtaaggggtaccattgggcacatagctcccgagtacctct 6065
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N FOR SEQ ID NO:
CHARACTERISTICS:
                                                        : (415) 781-1989
(415) 398-7040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meyerowitz, Elliot M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.6%;
                                                                                                                      A-60886/RFT/RMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124;
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US-07-717-331F-9
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US-07-717-331F-9
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Best Local S
Matches 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/07717331F Patent No. 5484905
                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/717
FILING DATE: June 19th 1991
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: June N
                                                                                                                        TELEFAX: (203)268-195
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4920 TTTGGACTCTGATTTTGAAGCCCCATGTTGCTGATTTTTGGGCCTTGCTAAGTTCTTAGTTGA 4979
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                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2571 base pair
                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: George M. Yahwak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4860 TCTTCACCATGATTGTTCACCATTGATCTTGCATAGAGATGTTAAGTCCAATAACATTCT 4919
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match 0.9%;
Local Similarity 58.9%;
hes 106; Conservative
                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
                                               STRANDEDNESS:
                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                               nucleic acid
DEDNESS: single
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25 Skytop Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5733 base pairs
                                                                                  2571 base pairs
                                                                                                                                         (203)268-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        June Nasrallah; Michael Nasrallah; and Joshua
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2434..5037
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                                                                                                                                                              (203)268-1951
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Encoded At The Self-Incompatability Locus
                                                                                                                                                                                                                                                                                          US/07/717,331F
                                                                                                                          9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 61.6; DB 3;
Pred. No. 6.6e-05;
0; Mismatches 74;
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Length 2571;

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                                                                                                                                                                   ; TOPOLOGY: 1:
; MOLECULE TYPE:
US-07-717-331F-1
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                   γQ
                                                                                                                                                                                                                                               TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2833 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 154; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/07717331F Patent No. 5484905
                                                           Query Match 0.9%;
Best Local Similarity 53.1%;
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                COMPUTER: MacIntesh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/717
FILING DATE: June 19th 1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION UNMER: 26,824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEPHONE: (203)268-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua APPLICANT: Stein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5049 gtaccatccttggaagaggtggatttggtaaggtgtataagggacgccttgctgatggct 5108
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MEDIUM TYPE: Floppy Disk
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5049 gtaccatccttggaagaggtggatttggtaaggtgtataagggacgccttgctgatggct 5108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: A Receptor Protein Kinase Gene TITLE OF INVENTION: Encoded At The Self-Incompatability Locus
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                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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Pred. No. 6.2e-05;
0; Mismatches 133; Indels
                                                           Score 61.2; DB 1;
Pred. No. 6.4e-05;
0; Mismatches 133;
                                                                                                     Length 2833;
                                                              Indels
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US-07-717-331F-4
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; MOLECULE TYPE:
US-07-717-331F-4
                                                                                                                                                                                                                                                                                                                                              TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2749 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Applic
Patent No. 5484905
                                                                                                                                                                       Query Match
Best Local Similarity
Matches 164; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua APPLICANT: Stein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
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COnnecticut
TSA
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NAME: GEOTGE M. YAHWAK
REGISTRATION NUMBER: 26,824
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1829 ATTCTTATCTCTTTGGTAAAACCCGAAGGTCTAAGCTAAATTGGAATGAG 1878
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5889 accattgtgatcccaagattatccatcgcgatgtaaaagctgcaaatatattattggacg 5948
                                                                                     1886 ATTGGCAAATGAGATTTGATATTATCAATGGTATTGCCCGAGGGCTTCTCTATCTTCACC 1945
                                                                                                                        5829 attggccaactagggagaggattgcactaggatcttctaggggcctatctaaattgcatg 5888
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/7
FILING DATE: June 19th 1991
CLASSIFICATION: 800
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ilarity 51.7%;
Conservative
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                                                                                                                                                                       ; Score 61; DB :; Pred. No. 7e-0; 0; Mismatches
                                                                                                                                                                                         DB 1; Length 2749; 7e-05;
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                                                                                                                                                                       Gaps
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US-08-265-628-1
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                                                                                                                                                                                                                                                                          TELEFAX: 312-707-9155
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2749 base pairs
                                                                                                                                                                                     TOPOLOGY: 1in
MOLECULE TYPE:
HYPOTHETICAL: 1
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APPLICATION NUMBER: US 0//0-...
FILING DATE: 03-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pochopien Ph.D., Donald J.
NAME: Pochopien Ph.D., 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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APPLICANT: Goring, Daphne
TITLE OF INVENTION: S-LOCUS RECEPTOR KINASE GENE IN A
TITLE OF INVENTION: SELF-INCOMPATIBLE BRASSICA NAPUS LINE
                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-707-8889
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                                                                                                                                                       ORIGINAL SOURCE:
PUBLICATION INFORMATION:
                                                                                   POSITION IN GENOME:
                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                  CHROMOSOME/SEGMENT:
                                                                                                    INDIVIDUAL ISOLATE:
                                                                                                                                     ORGANISM:
                             NAME/KEY:
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                                                                  S-locus
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Suite 3400
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Best Local Sim
Matches 154;
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APPLICANT: DORNER,
APPLICANT: SCHEIFL
APPLICANT: FALKNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14,
                                          APPLICATION NUMBER: EP 91 114 300.6
ETILING DATE: 26-AUG-1991
ETILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compa+40
                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
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TITLE:
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                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Alexandria
              TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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54; Conservative
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: ROTHSTEIN, STEVEN J.
THE S-LOCUS RECEPTOR KINASE GENE IN A
SELF-INCOMPATIBLE BRASSICA NAPUS LINE ENCODES
FUNCTIONAL SERINE/THREONINE KINASE
FUNCTIONAL SERINE/THREONINE KINASE
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1800 Diagonal Road,
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                                                                         30472/114 IMMU
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Pred. No. 8.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suite 500
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; CLONE: pTZgpt-F1s
US-08-232-463-14
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US-08-487-826B-13/C
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SEQUENCE CHARACTERISTICS:
LENCTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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APPLICANT: Sim, F
APPLICANT: Chitni
            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1187
                                                                                                                                                                                                                                             TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERVIHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1427 YYYYYYYGTACCAAA 1442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1307
                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               659 ggacctgnggacaaaa 674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 0.9%; Score 59.4; DB 1; Length 72
Local Similarity 1.6%; Pred. No. 0.00023;
hes 6; Conservative 229; Mismatches 141; Indels
                                                                                                                                              COUNTRY:
                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acctacctttttttctgtgttcccttttatgatatcacctgcttggaggcgtttagactt 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgctctggtggcttgtgtgcattttaggaatcttactctgttttttaatggagaaacgaa 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tcttcgtcagccttttctttccgatttttcccaagacaagattctttagttaatagttat 478

    Application US/08487826B
5993827

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                                                                                                                                                                            SSEE: Knobbe Martens Olson & F: 620 Newport Center Drive Newport Beach
DATE:
                                                                                                                                                              California
                                                                                                                                                                                                                                                                                                                                          Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
                                                                                                                                                                                                                                                                                                                           Peterson, David S.
10-SEP-1993
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Best Local Similarity 45.9%;
Matches 345; Conservative
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16212 TTTTTTCTAAAAAAAAAATGAACATATATGTGTATGTATATGTATTTAGGTATTAT 16153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16092 TATATATATGTATGTGTAAATGTGTATGTATGTATGGGTATATATATATATATATATGTA 16033
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                                                                                                                                                        15680 TTTTAATGTTT----TTTTTTTTTCTTCTTTTGTTTTTATTTTTTTTTATAATCATTTTTTT
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1174 taatttcttagctaagcggagcatctatcttaagtatctctactgaatttaagacataat 1233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Israelsen, Ned REGISTRATION NUMBER: 29,655 REFERENCE/DOCKET NUMBER: NITELECOMMUNICATION INFORMATION: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                           1474 tagttataagttaaaaaaaagcttcctattaattccaagatagaggttca-tttttatagt 1532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1354 taattitttattitttttttttttttatgttctttgcagaaagtttcttatggtcttttg 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1234 acatttttttaaaaaatctattagagtgttttttccgcacagcgcacatatatcttttt 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                         1593 acttttatggcgtcatgcagtgatcttgggaatgcagcattatctggtcaattggttcct 1652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1294 ctggtaattcagacaacctttctcccgacgataaaataatataagattaactccttgaac 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: lin
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                                                                                                                                                                                          cttggccagttgaaaaatttacaatacttgtaagaccatatcacttggaatgctttagtt 1712
                                                                                                                                                                                                                                                                                                                                            tcagcagttgttcggataatatctatgaagcacttaaaaggctgggcaatttttttgtta 1832
                                                                               TTTATATAAAAATTTTTTTTAATTTTTTTTTTGATAATCTTTTTTCATTTTTTATTCTATCA 15565
                                                                                                              tttatacagcacaatgctttcaatatctgttaaaagtgtgaaaaagttgactttctagct 1772
                                                                                                                                                                                                                                       TTATGTATATATTTTTTTTAACATTTTTTTAATTTTTTT---TTATTTTATGATATAT 15741
                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
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Pred. No. 0.0023;
0; Mismatches 394; Indels 13;
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RESULT 10
US-08-447-185-2
; Sequence 2, Application US/08447185
; Patent No. 5648599
; Patent No. 5648599
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; Sequence 83, Application PC/TUS9306251
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric and Rif
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TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US93-06251-83
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Best Local Similarity 52.2%;
Matches 120; Conservative
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 83:
                      GENERAL INFORMATION:
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FILING DATE: 19930630
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: D1G1g11o, Frank S.
REGISTRATION NUMBER: 31,34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                        1498
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEPEAX: 516-742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
  APPLICANT:
                                                                                                                                                        1558 ATAAAGTCTGATGTCTGGTCATTTGGAATTCTGCAAACAGAACTAGTAAC 1607
                                                                                                                                                                                                                                                                                                               1438 AAAATAGCAGACTTTGGTTTTAGCAAGGTTAATTGAAGACAATGAATACACAGCAAGACAA 1497
                                                                                                                                                                                                                                                                                                                                               5963 gttgtaggtgattttgggttagctaggctcatggattacaaggatacccatgttacgact 6022
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LENGTH: 4517 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                 gagaagaccgatgtctttggttatgggataatgctcctagagctcattac 6132
                                                                                                                                                                                                                                                                gctgtaaggggtaccattgggcacatagctcccgagtacctctcgactggaaagtcatca
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  Tanksley,
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Steven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 54; DB 6; Length 4517; Pred. No. 0.0032;
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Sequence 3, Application --,
Sequence 4, Application --,
Sequence 5, Application --,
Sequence 4, Application --,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Goldman Mr., Michael L.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)263-1000
TELEPAX: (716)-263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 159; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5124 aaaggettaaagaagaacgaaccacaggtggcgagetgcagtttcaaacagaagtggaaa 5183
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ATTORNEY/AGENT INFORMATION:
NAME: Goldman Mr., Michae
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APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 ATGGTGTCTTTGGGAAGGTTTACAAGGGTGTTTTGCGTGATGGAGCAAAGGTGGCCCTGA 205
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CLASSIFICATION: 800
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TOPOLOGY: unl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGAGATGATTCTAATTTATAAATACATGGAGAATGGGAACCTCAAGAGACATTT
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VVENTION: GENE CONFERRING DISEASE RESISTANCE
VVENTION: TO PLANTS BY RESPONDING TO AN AVIRULENCE GENE IN PLANT PATH
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Pred. No. 0.0021;
0; Mismatches 127;
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RESULT 12
PCT-US93-06251-77
; Sequence 77, Application PC/TUS9306251
; Sequence 77, Application PC/TUS9306251
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric and Rife, Jason P.
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
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; MOLECULE TYPE: DNA (genomic)
US-08-447-185-3
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SEQUENCE CHARACTERISTICS:
LENGTH: 2443 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 53.9%;
Matches 159; Conservative
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NAME: Goldman Mr., Michael L.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)263-1000
TELEPAX: (716)-263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5010 tttctctgcgagaattgcaagtcgcaacggatacttttagtacca-----tccttggaa 5063
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ADDRESSEE: Michael L. Goldman
                                                                                                                                                                                                                                                                                                                                                        386 ATGAGATGATTCTAATTTATAAATACATGGAGAATGGGGAACCTCAAGAGAGACATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 ATGGTGTCTTTGGGAAGGTTTACAAGGGTGTTTTGCGTGATGGAGCAAAGGTGGCCCTGA 268
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COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: New York
                                      ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCTCTCATTTTGCAGACATCCGCATCTGGTTTCATTGATAGGATTCTGTGATGAAAGAA
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USA
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Pred. No. 0.0028;
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RESULT 13
US-07-928-464-1
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 2647 base pairs
TYPE: nucleic acid
TYPE: nucleic double
                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/07928464
Patent No. 5367065
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: Mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 118; Conserv
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REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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NAME: DiGiglio, Frank S.
                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                             ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and ADDRESSEE: No. 5367065ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                       COUNTRY:
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                                                                                                                    19103
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3ER: 8586
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Pred. No. 0.014;
0; Mismatches 112;
                       Version #1.25
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APPLICATION NUMBER: UPPLING DATE: 19920810

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; LOCATION:
US-07-928-464-1
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PCT-US93-07347-1
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Best Local Similarity 52.8%;
Matches 134; Conservative
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Miller, Suzanne E.
REGISTION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-58-3100
                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                        APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene and
TITLE OF INVENTION: Mutations
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 19930805
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                           COUNTRY:
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; LOCATION:
PCT-US93-07347-1
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US-08-003-311B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application Patent No. 5444166
GENERAL INFORMATION:
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Best Local Similarity
Matches 134; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US
FILING DATE: January 1
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07
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REGISTRATION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UPN
TELECOMMUNICATION INFORMATION:
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                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSEE: Woodcock Washburn Kurtz Macklewicz and ADDRESSEE: No. 5444166ris
STREET: One Liberty Place - 46th Floor
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                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: and Mutations
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                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                             STREET: One Liberty CITY: Philadelphia
                                                                                                                                                                                                        ZIP: 19103
                                                                                                                                                                                                                          COUNTRY:
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LOCATION: 118..2583
US-08-003-311B-1
Search completed: June 23, 2000, 22:41:28 Job time: 40034 sec
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ATTORNEY/AGENT INFORMATION:
MAME: LOT1 Y. Beardell
REGISTRATION NUMBER: 34, 293
REFERENCE/DOCKET NUMBER: UPN-1:
TELEPHONE: 215-568-3100
TELEPAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3033 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FRANTER: CCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.8%; Score 50.8; DB 1; Length 3033; Best Local Similarity 52.8%; Pred. No. 0.015; Matches 134; Conservative 0; Mismatches 117; Indels 3
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length: 1000000
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   Result
                                                      Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.
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Query
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gb_est27: *
gb_est27: *
gb_est29: *
gb_est30: *
gb_est310: *
gb_gss1: *
gb_gss1: *
gb_gss1: *
gb_gss1: *
gb_gss2: *
gb_gss3: *
gb_gss3: *
gb_gss5: *
gb_gss6: *
gb_gss6: *
gb_gss7: *
em_gss7: *
em_gss1: *
gb_gss1: *
                              SUMMARIES
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Minimum Maximum

seq

Total number Searched:

Database :

Title: Perfect score:

Scoring table: Sequence: Run ğ

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RECEPTOR-LIKE KINASE.;, mRNA sequence. AW233982 N AW233982.1 GI:6566309 EST. Soybean. NISM Glycine max Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine. I (bases 1 to 532) Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M. Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,	ALIGNMENTS ALIGNMENTS BY MRNA C1028 Glycine max CDNA Clone GENOME SY. S' similar to TR:023921 023921 SOMATIC		Match Length DB ID 1
Query Match Best Local Similarity 79.98; Pred. No. 1.2e-42; Matches 319; Conservative 0; Mismatches 80; Indels 0; Gaps 0; acheophyta; Ledons; core Lionoideae; Qy 5860 atcttctaggggcctatctaaattgcattgtgatcccaagattatccatcgcga 5819	ID: BASE COUNT 1	FEATURES	McCann,R., Waterston,R. and Wilson,R. JOURNAL On Feb 18, 1999 this sequence version replaced gi:4297707. CONMENT Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST P

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 1
AW233982
LOCUS
DEFINITION

a

REFERENCE AUTHORS

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JOURNAL
MEDLINE
COMMENT
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AA738547
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                                                                                                          Query Match 3.7%;
Best Local Similarity 77.4%;
Matches 311; Conservative
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||||||||
                                                         agagcgtcagccatcagaacctccccctgattgg---ccaactagggagaggattgcact 5856
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aggatettetaggggeetatetaaattgeatgaeeattgtgateeeaagattateeateg 5916
                                    AGAGCGACAGCAATCTGAGCCACCTGTTAAGTGGGAAACAACAAGAAGACGGATTGCGCT 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 656)
Annen,F., Chang,J.-L., Paterson,A.H. and Stockhaus,J.
Characterization of 14 different putative protein kinase cDNA
clones of the C4 plant Sorghum bicolor
Mol. Gen. Genet. 259 (1), 115-122 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA738547 656 bp mRNA EST 17-AUG SBRLK5 Sorghum bicolor cv. TX430 leaf Sorghum bicolor ct SbRLK5 similar to protein kinase, highest similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Universitaetsstrasse 1, 40225 Duesseldorf, Tel: (49)-211-81-14953 Fax: (49)-211-81-14871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor-like protein kinases, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Stockhaus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Nov 29, 1993 this sequence version replaced gi:636097
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                                                                                                                                                                                                                       161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stockha@uni-duesseldorf.de
                                                                                                                                                                                                                 /note="Organ: leaf; Vector: Lambda ZAP II; Site_1: Site_2: Xho I; leaf cDNA library from green leaves. unidirectionally cloned: a 145 c 184 g 166 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sorghum
                                                                                                                                                                                                                                                                                    /db_xref="taxon:4558"
/clone="SbRLK5"
/clone_lib="Sorghum bicolor cv. TX430 leaf"
/dev_stage="green"
                                                                                                                                                                                                                                                                                                                                                                /organism="Sorghum bicolor"
/strain="cv. TX430"
                                                                                                                                                                                                                                                                                                                                                                                                                   ngth: 1100 Std Error: 0.00.
Location/Qualifiers
                                                                                                          Score 245.2; DB 38;
Pred. No. 1.1e-37;
O; Mismatches 88;
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Class: BAC ends
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1 (bases 1 to 1202)

newar,K., Buehler,E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 215-898-9384
Fax: 215-898-8780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis Thaliana Genome University of Pennsylvania
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                                  322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of Biology, University of Pennsylvania, Philadelphia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  jecker@atgenome.bio.upenn.edu
                                                                                                                                                       /organism="Arabidopsis to /strain="Columbia" /db_xref="taxon:3702" /clone="T2E10" /clone="I1b="TAMU" /clone_lib="TAMU" /
                           //sex="hermaphrodite"
/note="vector: BeloBACII; Site_1: HindIII;
/notIII; Produced by Rod Wing"
1 275 c 238 g 354 t 13 others
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Query Match
Best Local Similarity
Matches 397; Conserv

Conservative

3.7%;

Score 244.8; DB 84; Pred. No. 1.3e-37; 0; Mismatches 176;

Indels

19;

Gaps

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Length 1202;

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REFERENCE
AUTHORS
TITLE
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SOURCE
ORGANISM
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VERSION
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AI728030
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                                                                                     upland cotton.

Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

El (bases 1 to 555)
Elewitt,M., Matz,E.C., Davy,D.F. and Burr,B.
ESTs from developing cotton fiber
On Jun 5, 1998 this sequence version replaced gi:3187310.
Contact: Ben Burr
Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-396
Fax: 516-344-396
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AI728030.1
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BNLGH19629 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar
to (U93048)....somatic embryogenesis receptor-like kinase (Daucus
                                                          ll: burr@bnlux1.bnl.gov
primer: T3 Primer.
                                                                                                                                                                                                                                                                                                                                                                                    , mRNA sequence.
                             Location/Qualifiers
1. .555
/organism="Gossypium hi
/cultivar="Acala Maxxa"
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Best Local Similarity 62.2%;
Matches 432; Conservative
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            AI900110.1
EST.
                                                                AI900110 538 bp mRNA EST sc01a04.y1 Gm-c1012 Glycine max cDNA clone of Gm-c1012-871 5' similar to TR:023921 023921
                                                   RECEPTOR-LIKE KINASE. ;,
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/clone_lib="Six-day Cotton fiber"
/tissue_type="Immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="XLI-Blue"
/note="Vector: pBluescript II KS+"
a 100 c 147 g 162 t
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Pred. No. 2.2e-30;
0; Mismatches 119;
                                                      mRNA sequence.
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GENOME SYSTEMS CLONE ID:
1 SOMATIC EMBRYOGENESIS
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                                                                                                                                                                              gaacaattacattgacacagaagttgagcagcttattcaagtagcattactctgtaccca 6455
                                                           gggttcgccaatggagcggcctaagatgtcagaggtagtccgaatgcttgaaggtgatgg 6515
   AGGTTCCCCGATGGACCGACCTAAGATGTCAGAAGTGGTGAGAATGCTTGAAGGTGATGG
                                                                                                                                        AACCAACTATATAGAAACTGAGGTAGAACAGTTAATCCAGGTTGCACTACTCTGCACACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycine max
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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
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Location/Qualifiers
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seq primer: -40RP from G1bco
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314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from the apical shoots of 9 to 10 day old etiolated seedlings. The shoot tips including any emerged leaves were harvested for mRNA isolation. The CDNA library was prepared using the Stratagene pBluescript II XR CDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The CDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XLIO-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding."

13 a 105 c 142 g 138 t
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seedlings"
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/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID:
/clone_lib="Gm-c1012"
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73.6%;
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Pred. No. 2.4e-28;
0; Mismatches 90;
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Query Match 2.9
Best Local Similarity 69.8
Matches 259; Conservative
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                                                                         131 GAAGATTTTGAAGCAGTTGTCGGTGACTTTGGCCTTGCGAAGTTGGTGGATGTGAGGCGG 190
                                                                                                                                                                                                                                                                             11 GATTGGCCTCAAAGAAAAGAATAACCCTAGGTGCAGCATGTGGGCTGGAGTACCTTCAT 70
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acccatgttacgactgctgtaaggggtaccattgggcacatagctcccgagtacctctcg
                                                                                                      gaagaatttgaggctgttgtaggtgatttttgggttagctaggctcatggattacaaggat 6007
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to (U93048) somatic embryogenesis
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1 (bases 1 to 597)
Blewitt, M., Matt, E.C., Davy, D.F. and Burr, B.
ESTs from developing cotton fiber
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Fax: 516-344-3407
Email: burr@bnlux
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Seq primer: T3 Primer.
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/dev_stage="$ix days post anthesis"
/lab_host="XL1-Blue"
/note="Vector: pBluescript II KS+"
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/db_xref="taxon:3635"
/clone_lib="Six-day Cotton fiber"
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Matches 259; Conservative
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                                                   GAACATTGCAATCCTAAGATCATTCATCGAGATGTGAAGGCTGCAAATGTATTATTGGAT 130
                                                                                                                   GATTGGCCTCAAAGAAAAAAGAATAACCCTAGGTGCAGCATGTGGGCTGGAGTACCTTCAT 70
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 acccatgttacgactgctgtaaggggtaccattgggcacatagctcccgagtacctctcg 6067
                                GAAGATTTTGAAGCAGTTGTCGGTGACTTTGGCCTTGCGAAGTTGGTGGATGTGAGGCGG 190
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 703)
Blewitt,M., Matz.E.C., Davy,D.F. and Burr,B.
ESTs from developing cotton fiber
Unpublished (1999)
On Jun 5, 1998 this sequence version replaced g1:3188791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BNIGHI13383 Six-day Cotton fiber Gossypium hirsutum cDNA 5' sit to (U93048) somatic embryogenesis receptor-like kinase [Daucus carota], mRNA sequence.

A1729440
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Fax: 516-344-3407
Email: burr@bnlux1.bnl.gov
Seg primer: T3 Primer.
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Upton, NY 11973, USA
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148 c 180 g 186 t 1
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/cultivar="Acala Maxxa"
/db_xref="taxon:3635"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                            2.9%;
                                                                                                                                                                                                                             Score 191.8; DB 51;
pred. No. 2.4e-27;
0; Mismatches 112;
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                                                                               262;
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Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
euphyllophytes; Spermatophyta; Magnoliophyta; Solanaceae; Solanum;
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On May 7, 1998 this sequence version replaced g1:3121325
Contact: David Frisch
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Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cled862"
                                                                                                                                                                                                                        respectively.
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/tlssue_type="carpel"
/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XL1-Blue MRF/"
                                                                                                2.7%;
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Proc. Natl. Acad. Sci. U.S.A. 95 (22), 13330-13335 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Populus tremula x Populus tremuloides.
Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Core
euhyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
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A087p60u Hybrid aspen plasmid library Populus tremula
tremuloides cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                    Department of Biotechnology (KTH) Royal Institute of Technology (KTH) Technikringen 34, 5100 44 STOCKHOLM, Tel: +46 8 790 8287

Fax: +46 8 24 54 52
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Seq primer: CGTTGTAAAACGACGGCCAG
High quality sequence stop: 380.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                     Email: fredrik@biochem.kth.se
/note-"Vector: pBluescript SK; Site_1: SalI; Site_2: NotI Cambial region tissues, including developing xylem, the meristematic cambial zone and the developing and mature phloem, was harvested from 1.5 m actively growing trees. CDNA was prepared and cloned into lambda gt22a. DNA was isolated and subcloned into pBluescript SK using SalI and
                                                                                                                  /organism-"Populus tremula x Populus tremuloides"
/db_xref-"taxon:47664"
/clone_lib="Hybrid aspen plasmid library"
/tissue_type="Cambial region"
/dev_stage-"1.5 m actively growing tree"
/lab_host-"E.coli"
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BSTs from phosphate starved roots
Unpublished (1999)
On May 1, 1997 this sequence version
Contact: Maria J. Harrison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             barrel medic.
Medicago truncatula
Medicago truncatula
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; endicotyledons; core
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK
Tel: 580-223-5810
Fax: 580-221-7380
                                                                                                                                                                                                                                                                                                                                                                      'http://chrysie.tamu.edu/medicago'.
Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Developmental stage: phosphate starved; Date: 01/23/00; Submitted to the Database of Expressed Sequence Tags (dbEST) on 01/26/00; More information is available at
/clone_lib="rootphos(-)"
/tissue_type="roots"
/tissue_type="roots"
/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK or of the Initial RNA. The
CDNA was prepared from polyA+ enriched RNA. The
CDNA was directionally ligated into the Unizap XR vector
from Stratagene and packaged using Gigapack III Gold
                                                                                                                                                                                      /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="MHRP-24H06"
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                                                      On Dec 15, 1777
Contact: Xiaoying Lin
Che Institute for Genomic Research
The Institute for Genomic Rockville,
                                                                                                                                                                                                                                                                            Arabidopsis thaliana
Arabidopsis thaliana
Brasidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Endrophyta; eudicotyledons; core
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
euphyllophytes; Rosidae; eurosids II; Brassicales; Brassicaceae;
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                                                                                                                                                                                 1 (bases 1 to 714)
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
                                                                                                                                                                                                                                                                                                                                                                                             AQ969360.1 GI:6797061
GSS.
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 addtional information,
                                 Medical Center Dr.,
301 838 0200
301 838 0208
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74 c 107 g 124 t
                                                                                                                            1999 this sequence version
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Pred. No. 1.5e-25;
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http://www.tigr.org/tdb/at/at.html
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Class: shotgun
Minobe, Y. and Sasaki, T.
Rice CDNA from root
Unpublished (1995)
Contact: Yuzo Minobe
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
                                                                                                                                                                                                                                                                            D25047
RICR2976A
                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                               Oryza sativa
                                                                                                                                                                                                               EST.
                                                                                                              Poaceae; Oryza.
1 (bases 1 to 299)
                                                                                                                                                                                             Oryza sativa.
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/Clone_lib="LERG"
/clone_lib="LERG"
/note="Organ: Leaf; Vector: pUC19JK; Total genomic DNA was sheared to 0.4-0.7 Kbp before ligation."
a 177 c 112 g 220 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis tha
/strain="Landsberg erecta"
/db_xref="taxon:3702"
/clone="LERJM53"
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Pred. No. 1e-24
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                                                                                                                                                                                                                                 thale cress.
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; endicotyledons; core
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Japan 305
Tel: 0298-38-7441
Fax: 0298-38-7468
Email: minobe@rtcs0.riken.go.
                                                                                                                                                                                                                                                                                                                                                              survey sequence.
B27171
B27171.1 GI:2513137
                                                                                                                                                                                                                                                                                                                                                                                                            B27171 464 bp 1
T2E10TF TAMU Arabidopsis
                                             Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                      Arabidopsis Genomic Sequencing Unpublished (1997) Other_GSSs: T2E10TR
                                                                                                                                                                                              Arabidopsis.

1 (bases 1 to 464)

Rounsley,S.D., Kelley,J.M., Field,C.E., Craven,M.B., Adams,M.D.
Email: rounsley@tigr.org
Seq primer: M13-21
Class: BAC ends
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                                                                                                                            Contact: Steve Rounsley
                                                                                                                                                                                         Use of a BAC End Sequence
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/strain="Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
/clone="R2976_lA"
/clone_"R2976_la"
/clone_lib="Rice root"
/note="Prepared from seedling root. "
54 c 67 g 85 t
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               clones of Mol. Gen. 98409267
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                          1 (bases 1 to 991)
Annen,F., Chang,J.-L., Paterson,A.H. and S
CharacterIzation of 14 different putative
clones of the C4 plant Sorghum bicolor
Mol. Gen. Genet. 259 (1), 115-122 (1998)
                                                                                                                                                                                                             AA738544 991 bp mRNA EST 17-AUG-1998 SDRLK2 Sorghum bicolor cv. TX430 leaf Sorghum bicolor cDNA clone SDRLK2 similar to protein kinase, highest similarity to receptor-like protein kinases, mRNA sequence.

AA738544 AA738544.1 GI:3421469
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                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                               Sorghum bicolor
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Similarity 65.6%;
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Location/Qualifiers
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/note="vector: BeloBACII; Site_1: HindIII; Site_2:
HindIII; Produced by Rod Wing"
87 c 115 g 143 t
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="T2E10"
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1993 this
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sequence version replaced gi:636080
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Pred. No. 1.1e-23;
0; Mismatches 135
                                                             and Stockhaus, J.
ative protein kinase
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Best Local S
Matches 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240;
                                                                                                                                                                                                                                             AA738545 1435 bp mRNA EST 17-AUG-1998 SDRLK3 Sorghum bicolor cv. TX430 leaf Sorghum bicolor cDNA clone SbRLK3 similar to protein kinase, highest similarity to receptor-like protein kinases, mRNA sequence.

AA738545
1 (bases 1 to 1435)
Annen, F., Chang, J.-L., Paterson, A.H. and Stockhaus, J.
Characterization of 14 different putative protein kinase
clones of the C4 plant Sorghum bicolor
Mol. Gen. Genet. 259 (1), 115-122 (1998)
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Universitaetsstrasse 1, 40225 Duesseldorf, Germany
Tel: (49)-211-81-14953
Fax: (49)-211-81-14871
                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Sorghum
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/note="0rgan: leaf; Vector: Lambda ZAP II; Site_1:
Site_2: Xho I; leaf cDNA library from green leaves,
unidirectionally cloned"
a 194 c 293 g 251 t
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fuer Entwicklungsbiologie und Molekularbiologie
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                       attactggacagagggcttttgatcttgctcgccttgcgaacgatgatgatgt 6180
                                                                                                                                                                                                                                     gaagaatttgaggctgttgtaggtgattttgggttagctaggctcatggattacaaggat 6007
                                                                                        actggaaagtcatcagagaagaccgatgtctttggttatgggataatgctcctagagctc 6127
                                                                                                                                                                                                                                                                                        gaccattgtgatcccaagattatccatcgcgatgtaaaagctgcaaatatattattggac 5947
GTCACTGGTCAGCGTGCCATAGACTTTTCACGTCTGGAGGAAGAAGATGATGT
                                                                       ACTGGGAAGTCATCCGAGAGAACCGATGTTTTTGGTTACGGCATAATGCTTCTCGAGCTA
                                                                                                                                            ACATCTGTGGCTGCTCAGGTCCGTGGAACTATGGGTCACATTGCCCCCTGAATATTTGTCC 1041
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Tel: (49)-211-81-14953
Fax: (49)-211-81-14871
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on Nov 29, 1993 this sequence version replaced g1:636085
Contact: Stockhaus J
Institut fuer Entwicklungsbiologie und Molekularbiologie
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Similarity 67.7%;
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/clone="SbRLK3"
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/dev_stage="green"
/note="Organ: leaf; Vector: Lambda ZAP II; S
/ite_2: Xho I; leaf cDNA library from green
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Maximum DB seq length: 1000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.

1 (bases 1 to 1815)
De, V.S., Schmidt, E.D., Van.H.G. and Hecht, V.F.
PRODUCTION OF APOMICTIC SEED
PRODUCTION OF APOMICTIC SEED
PAtent: WO 9743427-A 20-NOV-1997;
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Sequence 2 from Patent W09743427.
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A67797.1 GI:4756623
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gt 1560	aattacattgacacagaagttgagcagcttattcaagtagcattactctgtacccaggc	1501	Qy
AC 1500	GTTAAAAGCCTTTTGAAAGAGAAAAAGTTGGAGATGCTGGTCGATCCTGACCTGGAGAA	1441	ДD
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gg 1440	agagagettttgatettgetegeettge	1381	δ
> —	TCATCAGAGAAGACCGATGTCTTTGGTTATGGGATTATGCTCTTAGAGCTCATTACTGG	32	Db
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AG 1320	ACAACTGCTGTAAGGGGTACCTTGGGCTACATAGCTCCCGAGTACCTCTCGACTGGAAAG	1261	đđ
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TT 1260	GAGGCTGTTGTAGGTGATTTTGGGTTAGCTAGGCTCATGGATTACAAGGATACCCATGT	1201	Дb
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T 960	CTGCAGTTTCAAACAGAGGTGGAAATGATTAGCATGGCTGTGCATCGAAATCTTCTGCG	901	망
jt 960	tgcagtttcaaacagaggtggaaatgattagcatggctgtgcatcgaaatcttctgcg	901	Qy
e 900			Db
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T 840	GATACTTTTAGTACCATACTTGGAAGAGGTGGATTTGGTAAGGGTGTATAAGGGACGCCT	781	В
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·9 780	cagaagtgcaccttggtcaactgaagaggttttctctgcgagaattgcaagtcgcaac		Qy
C 720	GCATGGTGGCGGAGAAAACCGCGAGAACATTTCTTTGATGTGCCAGCTGAAGAGAG	661	Дb
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T 660	ATTGCTGGGGGAGTAGCTGCTGCTGCTTTACTGTTTGCTGCACCTGCAATGGCATT	601	뮻
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A 540		8	밁
	tttatgtggacccgtaactgggaggccctgccctggatctcccccattttcgccacc	œ	ρy
G 480	CCAGTACCGGATAATGGCTCATTTTCTTTGTTTACACCTATCAGTTTTGCCCAATAATTT		В
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Schmidt, E.D., Guzzo, F., Toonen, M.A. and de Vries, S.C.
A leucine-rich repeat containing receptor-like kinase marks somatiplant cells competent to form embryos plant cells competent to form embryos pevelopment 124 (10), 2049-2062 (1997)
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Submitted (12-MAR-1997) Molecular
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Sequence
A67796
A67796.1
Daucus carota
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
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1 (bases 1 to 6695)
De, V.S., Schmidt, E.D., Van, H.G. and
PRODUCTION OF APOMICTIC SEED
Patent: WO 9743427-A 20-NOV-1997;
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1182 c 1243 g 2421
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Pred. No. 2.7e-115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-JUN-1999) Plant Gene Expression Center, 800 St., Albany, CA 94710, USA On Jun 17, 1999 this sequence version replaced gi:4996902. The sequence of BAC F23M19 from Arabidopsis thaliana chrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vysotskaia, V.S., Schwartz, J.R., Yu, G., Toriumi, M., Lenz, C., Liu, S., Lee, J., Liu, A., Li, J., Kremenetskaia, I., Luros, J., Gonzalez, A., Altafi, H., Araujo, R., Chao, Q., Conn, L., Conway, A.B., Dunn, P., Hansen, N., Huizar, L., Kim, C., Palm, C., Rowley, D., Shinn, P., Walker, M., Davis, R.W., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Davis, R.W., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Davis, R.W., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Davis, R.W., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Davis, R.W., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Ecker, J.R., Federspiel, M. Walker, M., Ecker, J.R., Federspiel, M. Walker, M., Ecker, M., 
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/gene="F23M19.1"
complement(join(796...1116,1205...1271,1349...
1506...136,1794...1850,1999...2047,2166...22
2771...2893,2990...3079,3154...3254,3332...33
3638...3891))
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/protein_id="AAD39602.1"
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EFHFLGDAILRYFRCRVNLIYNPDSPLYHGVVSRCQILHGRYVATPWLASPHIQTCFL
NFHGLPPYFTYTRQLFLTSDGGTIALDWLTNSDYLDGSLHNKSEITKEDTTPIAVVIP
                                       GLTSDSSSAYLKHLAYDTAKTGWNVYISNHRGLGGVSVTSDCFYNAGWTDDIRVVLDY
LQHKYPRAPLFAIGTSIGANVLVKYLGEEGEKTPLRGAVAICSPWDLLIGDRFICRTL
KQKLYDKALTIGLQGYAQLHEPQFLRLANWEGIKKSRSIRDFDNHATCLVGKFETVDT
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/note="Contains a
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/cultivar="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
/YRKSSSTQYVGNVAVPLLCISALDDPLCTKEAIPWDECRANKNIVLATTNHGGHLAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF|00561 alpha/beta hydrolase fold
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1 BAC F23M19 sequence, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expression Center,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thaliana chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2251,2468.
.3393,3467.
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                                                                                                                                                                                                                                       Sg
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/note="Contains similarity to gi|479356 protein kinase from Zea mays, is a member of the PF|00954 S-Locus glycoprotein family and contains a PF|00069 Eukaryotic protein kinase domain."
                                                                                                                                                                                                                                                                            TGWNAFTTSKKLVAGDVIVFVRGETGELRÜGIRRARHQQĞNIPSSIVSIDCMRHGVVA
SAKHAFDNQCMFTVYK PRSSKFIVSYDKFLDAVNINKFNVGSRFTMRLEGDDPSERRC
FGTIIGVSDFSPHWKCSEWRSLEVQWDEFTSFDFDKKYSPWDIEHLMPAINVPRSFLL
KNKRLREVNEIGSSSKHLLPFILTQGQENEQLSVASPMNISLRYRDATEDAMNPSKLL
MSYPVDPMPKLINYNNQMYTEMEENITTKTGTNFRLFGVTLDTPFVIKDPIEEIGSEIS
KLTEGKKFGLSQTLRSPTEIQNKQFSSSRTCTKVQMQGVTIGRAVDLSVLNGYDQLIL
ELEKLFDIKGQLQTRNQWEIAFTDSDEDKMLVGDDPWPEFCNMVKKIFIQKRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVYYFPQGHIELVSSLSLSLFLFSFSLHLFSLSLLSLSVETSTREELNELQPICDLPS
KLQCRVIAIHLKVENNSDETYAEITLMPDTTQVVIPTQNENQFRPLVNSFTKVLTASD
TSAHGGFFVPKKHAIECLPSLDMSQPLPAQELLAIDLHGNQWRENHNYRGTPQRHLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(23307...2355,23431...23627,23656...23751,23850...2:
24002...24145,24225...24309,24401...24491,24571...24735,
24842...24955,25045...25117,25210...25348,25453...25865,
25953...26140,26231...26279)
//gene___F23M19.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /TITEDOURMLEDVERMED OF THAT WISHTLINNASDLNSHSGESGIK
/TITEDOURMITSESSEPIVSSGSHPONIEDGIPKLSRVLSOKSRSTKSRQAA
VAKVSEVSLIGRAGTMGLGKAVDUDTLGSSGSHPONIEDGIPKLSRVLSOKSRSTKSRQAA
VAKVSEVSLIGRAGTMGLGKAVDUDTLGSSGFVONILISGGFSSATTVKGNKISLISF
EVANTIVKGAKLMHSLSKOSITHLKEVVLFSEGVQNLISKODDELLAIATATELKSQKK
PUTLVVTQRDLYHELHALDRFEQDYQRKIQEEENPSTAQRGVGDTLAILRTELKSQKK
HVRNLKKKSLWSRILEEVMEKLVDVVHFLHLEIHEAFGGADDKSPANDPINHKKLGS
AGLALHYANIITQIDTLVSRSSTMPASTRDALYGGLPSGSEKSANGRPAGOTILAIDTLH
HADKEKTEAYILDWLYMPATNTTKAHHGFGGVGEMASSGSEKSANGRPAGOTILAIDTLH
HADKEKTEAYILDUVAKHHLVTQVRATTGYGLRSPVKSPIRSPNQKTIQLSSGSHNP
SMGLPILTTEDQEMLEDVSKRKTPGISKSGEFETVAKARLCKHRLSKSSSHSPMMG
SMGLPILTTEDQEMLEDVSKRKTPGISKSGEFETVAKARLCKHRLSKSSSHSPMMG
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HSLKQTVTAALLRMOPHDCFYNVRKLLLCVFYVGCDASILIDSTPERDSEKSAEANV 
SVRGFEIIDEVKKELEIVCPKTVSCADIVTLAKTRDSIALAGGLNVTNMVALIGGGHSV 
GVAHCSLFQDRLKDPKMDSKLKAKLONTCRGPNDPSVVLDQMTPLFDNMQIXQIKSQ 
RGILRIDQNLGLDDSTSRIVSNFALNETLFGERFAEAMQIMGEIKVLTGNSGEIRTNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Similar to gb|AF082176 auxin response factor 9 from Arabidopsis thaliana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="F23M19.4"
join(23307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(5693. .6732)
/gene="F23M19.2"
                                                                                                                                                  /gene="F23M19.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
/protein_id="AAD39615.1"
/db_xref="GI:5091627"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMMKNKKDTFSTRRPSSVPIIDFDIDRMKALDVIDRVDTIRSL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
/product="F23M19.3"
/protein_id="AAD39604.1"
/db_xref="GI:5091616"
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/protein_id="AAD39603.1"
/db_xref="GI:5091615"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
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                                                                                                                                                                                                                                                complement(28888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Similar to gb|X98322 peroxidase (prxr10) from
Arabidopsis thaliana."
                                                                                                                                                                                                                 /gene="F23M19.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MESGNVVNAQPELSGIIDGSKSYVYEQLWKLCAGPLCDIPKLGE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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Query Match
Best Local Similarity
Matches 828; Conserv
                                                                                                     73350 TTCTGTGATGCAGCCGAAGAGGCCCTGAGGTTCACTTGGGGCAGCTTAAGCGGTTCTCT 73291
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757 ctgcgagaattgcaagtcgcaacggatacttttag-----taccatacttggaagaggt 810
                                                                                                                                            697 tttgatgtgccagctgaagaggacccagaagtgcaccttggtcaactgaagaggttttct 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id-"AAD39606.1"
/db_xref-"GI:5091618'
/translation-"MINYRHIVECLCVMVVVDSRLTEYLAAIEQVDEIVKIVLPIVGR
FDPEEFYTSWOGUNPCEWFGTNCLEGIIIGISFISLMLIGTISPHFADLTSLEVIDLS
HNRLKCTIPFEITKLKNLTIVDVSYNQLHGEVPRVRGIVILTERNPNIESTCLLVPSP
TRNKNKETYVVLLIGILVGLVVAGGASFGFYLKRIRKDFKRLGEPNEAVTLTQQQSSD
ESLYSDESYLTSIOLQYRVLRRESWVSKGPLLLTRQLKTNQNPHLPYM*
40313...42256
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TSYYKYCGPVVANTLERATKGDDNNSKYHLMIYAVANIAGLLGLYAVEIGLWWCCCRK
NPRFGTLSSHYTLLEYASGAPVQFTYKELQRCTKSFKEKLGAGGFGTTVFRWCCCRK
VAVKOLEGIEQGEKQFRMEVATISSTHHLMLVRLIGFCSQGHRFLLVYEFMRWGSLDN
FLFTTDSAKFLIWEYRF NIALGTAKGITYLHEECRDCIVHCDIKPENILVDDNFAAKV
SDFGLAKLLNFXDNRYMSSYRGTRGYLAFFWLANLFITSKSDYSYSYGHYLLELVSGK
RNFDVSEKTHNKKFSIWAYLEFEKGNYKAILDFTRLSEDGYTUMFDYNKWYNTSFWCIQ
EQDPLQRPTMGKTVQMLEGITEIKNPLCPKTISEVSFSGNSMSTSHASMFVASGPTRSS
SFSATTSFQTMGITSSGPASTRISEGSMLGS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(36027. .36827)
/gene="F23M19.6"
complement(36027. .36827)
/gene="F23M19.6" .36827)
/gene="F23M19.6" two PF|00560 leucine-rich repeat domains."
/codon_start=1
/cvidence-not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYSFQLERSGNLTLRWITSAIYWNHGLNSSFSSNLSSPRLSLQTNGVVSIFESNLLG
GAEIVYSGDYGDSNTFRFLKLDDDGNLRIYSSASRNSGPVNAHWSAVDQCLVYGYCGN
FGICSYNDTNFICSCPSRNFDFVDVNDRRKGCKRKVELSDCSGNTTMLDLVHTRLFTY
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PNSTFSVSFVPSPSPNSFLAAVSFAGSVPIWSAGTVDSRGSLRLHTSGSLRLTNGSGT
TVWDSKTDRLGVTSGSIEDTGEFILLNNRSVPVWSSFDNPTDTIVQSQNFTAGKILRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(43028. .48860)

/gene="F23M19.8"

complement(join(43028. .43288,43400. .43672,43778. .45067,
45156. .45311,45523. .45649,45915. .46249,46361. .47119,
47284. .47637,47725. .47869,48023. .48613,48703. .48736,
48815. .48860))

/gene="F23M19.8"

/note="Contains similarity to gi|836774 FAB1 protein from
Saccharomyces cerevisiae genome gb|D50617."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MVPKIASMASTRPLCSIPSIFLSFSLLFVVSLLFFFSNSLISNP NPSISHNTLONGINVTVAELFRSLNYGLIDKTWSSSFDSRIPSDPDHFTRKTHSPDK YPSYFENFLIKOYSAEYWIMGDLETSPEKRIGSFAKKVFESDADVVFVPFATLSAE MELGNGKGSFRKKSGNEDYORORQVLDFVKNTKAWKRSNGRDHVFVLTDPVAMMHVRE EIALSILLVVDFGGWFRQDSKSSNGTSLPERIQHTQVSVIKDVIVPYTHLLFRLDLSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="F23M19.7"

/gene="F23M19.7"

/gene="F23M19.7"

/codon_start=1

/evidence=not_experimental

/product="F23M19.7"

/protein_id="AAD39607.1"

/protein_id="AAD39607.1"
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/db_xref="GI:5091617"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KWLANHLGRFSEREKETLRSRIAKVQSVFVYDNGHADGIGPIEPNGAVNHIWKKVQQK
VPMVKEAVIRERRKPAGASVPLRCQCI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NQRRHSLLYFKGAKHRHRGGLIREKLWDLLVNEPGVVMEEGFPNATGREQSIRGMRNS
EFCLHPAGDTPTSCRLFDAIQSLCIPVIVSDTIELPFEGIIDYSEFSVFASVSDALTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
/protein_id="AAD39608.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                   23.9%;
                                                                                                                                                                                                                                Score 434; DB 8; Pred. No. 4.3e-87; O; Mismatches 245;
                                                                                                                                                                                                                                                                                                  Length 88401;
                                                                                                                                                                                                                                   Indels 217;
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JOURNAL REFERENCE
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AUTHORS
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ORGANISM
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KEYWORDS
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Direct Submission

Submitted (11-MAR-1999) MIPS, at the Max-Planck-Institut fuer submitted (11-MAR-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schuelle@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euqhyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.

1 (bases 1 to 96475)

Bevan, M., Rose, M., Hempel, S., Entian, K.-D., Hoheisel, J., Mewes, H.W., Mannhaupt, G., Mayer, K.F.X. and Schueller, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosome viewed at: http://websvr.mips.blochem.mpg.de/proj/thal/.
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2 (bases 1
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/note-"similarity to Caenorhabditis elegans cosmid, gene T16G1.11, prD:e134936; contains EST gb:T20620, N65143, 745799, H36819, R65238, N37318"
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SLIVLSHYLETGREQQFWDEAAKNRHILEAVPGFEQAIQAYASHLLSLSYQKVPRSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="F17M5.10" complement(2377. .2571)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Arabidopsis thaliana"
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complement(3099.
/number=3
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LPSNHSASLHQQPKSYKPRRYIPQTSBRTLDAPDIVDEVLNNSEVQLUBASANRQLR
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TLKGGHQSRVSSLAWNNHILTTGGMDGLIINNDVRIRSPIVETYRGHTQEVCGLKWSG
SGQQLASGGNDNVYHHWDRSYASSNSTTQWLHRLEBHTSAVKALANWCPFQANLLATGG
                                                                                                                                                                                                                                               complement(join(7856 ...7999,8104 ...8685,8767...9139...9417,9803 ...9901))
9139 ...9417,9803 ...9901)
/note="strong similarity to WD-repeat protein carota, PII:92253631; Contains Trp-Asp (WD-40) signature [VLAIALDHTVYLWDA] [TGGGGGDRTIKFWNT]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNVVHIWDRSVASSNSTTQWLHRLEEHTSAVKALAWCPFQANLLATGGGGGDRTIKFW
NTHTGACLNSVDTGSQVCSLLWSKNERELLSSHGFTQNQLTLWKYPSMVKMAELTGHT
SRVLYMAQSPDGCTVASAAGDETLRFWNVFGVPETAKKAAPKAVAEPFSHVNRIR"
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complement(7856. .7999)
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/gene="F17M5.20"
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                                              21.9%;
ilarity 64.1%;
Conservative
                                                                                                                         /gene="f17M5.50"
12884. 14176
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LEENDLLVFKFFHGVSEFEVLVFDGQTLCEKFTSYFVRKCGHAEKTKGIIDFNATSSRS
EKRHFXPEDDVETTPNQGLVISFFVDNELEDLIDIDLDETDIDKLINFLLVASRTGYEQE
EHINSDIDTABAQLFVISFTSYRVSEGKFYLSGFKKMRLTTRQEVVMQVDQTKWEMK
LSLAKRAISPDGFLVFMKRSHVYSKCFLTIFYKWCVKNMLTTRQEVVMQVDQTKWEMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(10668. .10967,11056. .11159,11587. .12457, 12511. .12621))
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/number=5
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SHVNRIR"
                                                                                                                                                                                                                                                                                        /note-"strong similarity to Arabidopsis thaliana chromosome II BAC (gene T6A23.21), PID:g3786013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(11056.
/number=2
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1647	88 gaggtagtccgaatgcttgaaggtgatggccttgcagaaaagtgggacgagtggcaaaaa	158	Оy
50081		5014	
1587	28 cttattcaagtagcattactctgtacccagggttcgccaatggagcggcctaagatgtca	152	DP GA
50141		5020	
1527	8 ttggagatgctggtcgatcctgacctggagaacaattacattgacacagaagttgago:	146	Db Qy
50201		5026	
1467	0	144	Db
50261		5032	Db
1440 50321	9 ttgttggattg	38	Qy Db
1428	9 ctcattactggacagagagcttttgatcttgctcgccttgcgaacgatgatgatgtt	36	Db Qy
50381		44	
1368 50441)) togactggaaagtcatcagagaagaccgatgtctttggttatgggattatgctcttagag 	50	D Qy
1308	9 gatacccatgttacaactgctgtaaggggtaccttgggctacatagctcccgagtacctc	124 5056	Dy Db
1248	9 gacgaagaatttgaggctgttgtaggtgattttgggttagctaggctcatggattacaag	118	Db
50561		5062	Db
1188	9 catgaccattgtgatcccaagattatccatcgtgatgtaaaagctgcaaatatattattg	112	оу
50621		5068	Оу
1128	9 cttgattggccaactaggaagaggattgcactaggatctgctagggggctttcttatttg	06	Ду
50681			Дъ
1068 50741	agagogtcagccatcagaacctccc 	5080	D Qy
08	GTATCTCTCATCTTGTGCCTTTTTCTTTGACTGCAATATTTCCGTCCAATGGTTGCCTTT	98	Дb
1044		104	Qy
1044 50861	<pre>gagcggcttcttgtatatccatacatggctaatggaagtgttgcgtcgtgtttaag </pre>	986 50920	Оy
985 50921	6 tgattagcatggctgtgcatcgaaatcttctgcgtctacgtggtttctgcatgacaccaa	926 5098	Db Qy
925	agaagaacgaacaccaggtggtgagctgcagtttcaaacagaggtggaaa	866	Qy
50981		51040	db
865 51041	gaggtggatttggtaaggtgtataagggacgccttgctgatggctcacttgtagcagtta	806 51100	DP QA
805	2 tttctctgcgagaattgcaagtcgcaacggatacttttagtaccatacttggaa	752	Qy
51101		51160	Db
51161	ATTACCGTCTTTTTGCAGCTGAAGAGGACCCAGAAGTTCATTTAGGACAACTGAAGAGGT	51220	Db

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     tgcatcgaaatcttctgcgtctacgtggtttctgcatgacaccaacagagcggcttcttg
                                    AGCGAACTCCAGGTGGAGAGCTCCAGTTTCAAACAGAAGTAGAGATGATAAGTATGGCAG
                                                        aacgaacaccaggtggtgagctgcagtttcaaacagaggtggaaatgattagcatggctg
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Submitted (02-NOV-1999) Plant Gene Expression Center,
Street, Albany, CA 94710, USA
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Liu,S.X., Lee,J.M., Sakano,H., Yu,G., Jhaveri,A., Lenz,C.,
Liu,S.X., Chin,C., Chiou,J., Choi,E., Gonzalez,A., Howng,B.,
Toriumi,M., Chin,C., Chiou,J., Vaysberg,M., Altafi,H., Brooks,S.,
Koo,T., Li,J., Liu,A., Pham,P., Vaysberg,M., Altafi,H., Brooks,S.,
Buehler,E., Chao,Q., Conn,L., Conway,A.B., Hansen,M.,
Johnson-Hopson,C., Khan,S., Kim,C., Lam,B., Nguyen,M., Palm,C.,
Shinn,P., Tambunga,G., Davis,R.W., Ecker,J.R., Federspiel,N.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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10, 1999 this sequence version location/Qualifiers
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                                                                  agaagtcatccatcaagacgtagaattagctccacatcgaacttctgaatggatcctaga 1709
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             ctcgacagataacttgcatgcttttgaattatctggtccaagataaacagcatataaa 1767
                                                                                                      AGTTGTAAGGATGCTGGAAGGAGGGGCTTGCGGAGAAATGGGACGAATGGCAAAAAGT 80997
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                                                                                                                                                           GATACAAGTGGCGTTGCTATGCACGCAAGGATCACCAATGGAAAGACCAAAGATGTCTGA 80937
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                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/ERNAscan-SE/). Simple repeats were lidentified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/M/RepeatMasker.html). Genes are numbered from the top to the bottom of the chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thale cress.
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC006436 AE002093
AC006436.4 GI:6598565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter, J.C.
                                                                                                                                                                                                                                                                   This work was supported by the N
Department of Energy and the US
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(http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              We thank the CSHL/WashU/ABI consortium for sequencing BAC clones
                                                                                                                                                                                                                                                                                                                                                                       database support.
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                                                                                                                                                                                                  all correspondence to:
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/organism="Arabidopsis
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/db_xref="taxon:3702"
/chromosome="2"
                                                                                                                                        .65899
                                                                                                                                                                                                                                                                                                       supported by the National Science Foundation,
                                                                                                                                                                     /Qualifiers
                                                                                                                                                                                                  at@tigr.org
                                                                                                                                                                                                                                                                      Department of Agriculture.
                                                                                                    thaliana'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     please see the TIGR web site
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                                                                                                                                 /pseudo 29450. .
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//gene="At2g13690"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="magsstshdsgpoglmrrpsrsaattysievedhevvpaslgti

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mgeaanirfweeclcyifhnmayelhgllagnysivtgenikpsyggddeaflrkvit
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/gene="At2g13660"
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/note="F13J11.2; predicted by genscan and genefinder"
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/10in(3349. .4230,4792. .4928,5629. .5755,5848. .5997)
/10in(3349. .4593,4792. .4928,5629. .5755,5848. .5997)
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spprnlylclrlyllafchrspeeieqdedsnssysvpinrinlinpprrtdalnkpf
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LEVLAANSUVTPGGLTAEEKKCSSSSSGLKNTCRIEVCDVENLGYPRETDEEEKLRRLLGIY
NVIIKKFMTMGVYRAIDVLEVAAGIKESRAVLSCLKYLEAVPWTEDEEEKLRRLLGIY
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complement(<14929. .>17114)
/gene="At2g13690"
/note="F13J11.4; predicted by
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/note="pro-
                                                                                                                                                                                                                                                                          complement(18082.
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WFSKHGTECPNLSKAFQIWWRRSFLRGVESSTCR"
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LEIMIDREIAEEFVEIWGKQRRLVEMHERVSPMVRYEVSRVTGAIFIAMGKRRVQCGG
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/note="Sequence from clone F13J11"
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Best Local Similarity 63.8
Matches 720; Conservative
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32232...>33473
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ytes; Spermatophyta; Magnoliophyta; Liliopsida orghum. 1 to 2278)	SBRLK1 2278 bp mRNA PLN 24-JUL-1999 Sorghum bicolor mRNA for protein serine/threonine kinase RLK1. Y14600 Y14600.1. GI:5596995 protein serine/threonine kinase; RLK1 gene. sorghum. Sorghum. Sorghum bicolor Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophy	GGAAGGAGATGGTTTAGCTGAGAATGGGAAGAATGGCAAAAGGAGGA 54694	tgaaggtgatggccttgcagaaaagtgggaacgagtggcaaaaagtaga 1652	GTCAGAAGTAGTGAGAATG	actctgtacccagggttcgccaatggagcggcctaagatgtcagaggtagtccgaatgct 1604	GAGCAGCI	tootgacotggagaacaattacattgacacagaagttgagcagcttattcaagtagcatt 1544	 TAGGTGAAAGAGGTT	gttggattgggttaaaagccttttgaaagagaaaaagttggagatgctggtcga 1484	GTTCCCGATCATATTTTTGAGTTCAAAACTGTTATTTTGCAATAAAGAAGAGTGTTTCTT 54466	1431	TTGCAAATGATGATGATATCA	ttgctcgccttgcgaacgatga	TGTTTTTGGGTACGGGGTCATGCTTCTCGAGCTCATCACTGGACAAAAGGCTTTC	ggttatgggattatgctcttagagctcattactggacagagagcttttg	CCATATAGCGCCCGAGTACCTCTCGACAGGAAAATCTTCTGAGAAA	gctcccgagtacctctcgactggaaagtcatcagagaaga	ATTITGGGCTCGCAAAATTAATGAATTATAATGACTCCCATGTGACAACTGCTGTAC	gggttagctaggctcatggattacaaggatacccatgttacaactgctg		ıtcytyatytaaaayctycaaatatattattggacgaagaatttgagyct	TACATGATCATTGCGACCAAAAAATCA	tgcatgac	TICTATITIAGAGCGTCCTGAAGGCAATCCAGCACTTGATTGGCCCAAAAAAGCATAT 54046	agagogtcagccatcagaacctccccttgattggccaactaggaagagggt 1094	CCTATAGTATTGTTTGACTGGTTTTTGATTGGTCAGTTGGGAAGTATCTTATCCTTGATT 53986	1044	TTTATCCCTACATGGCTAATGGAAGTGTTGCTTCTTGTTTAAGAGGTACCACAACTTTGT 53926	atc	TICATAGGAACTTGCTTCGGCTTCGTGGCTTTTGCATGACTCCAACTGAAAGATTACTTG 53866

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TITLE
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Best Local Similarity
Matches 826; Conserv
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                                                                                           gctcattttct---ttgtttacacctatcagttttgccaataatttgaatttatgtgga-
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     -cccgtaactgggaggccctgccctggatctcccccattttcgccaccacctccgttcat 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stockhaus,
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164 . 235
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233. .2020
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Pred. No. 4.9e-61;
0; Mismatches 634;
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                      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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De, V.S., Schmidt, E.D., Van, H.G. and PRODUCTION OF APOMICTIC SEED Patent: WO 9743427-A 20-NOV-1997;
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                                                                                                                                          Direct Submission Submitted (06-MAY-1998) to the DDBJ/EMBL/GenBank databases. Yasukazu Nakamura, Kazusa DNA Research Institute, Laborator Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935, Fax:+81-438-52-3934)
                                                                                                                                                                                                                                                                                                                              Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
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                                                                                                                              2 (bases 1 to 134784)
Sun, H., Wohldmann, P., Johnson, D. and The sequence of A. thallana F17123
Unpublished (1999)
3 (bases 1
                                                        Direct Submission
Submitted (17-JUN-1999)
University, 4444 Forest
Submitted by:
                                                                                                                                                                                                                                                                          Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Arabidopsis thaliana B/
AF160182
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                                                                                                                                                                                                                 Washington University Genome Sequencing Center The A. thaliana Genome Sequencing Project
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Department of Genetics, Wash
St. Louis, MO 63108, USA
e-mail: rwilson@watson.wustl
                                          Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                           134784 bp I
thaliana BAC
                                                                       Department of Genetics, Washington Park Avenue, St. Louis, Missouri 63108,
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MAPPING: Clones were assigned to the YAC map by hybridization by M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted by M. Marra, WashU, to pick the best candidates for sequencing.

NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone

NEIGHBORING COSMID INFORMATION

8 멇 δÃ 밁 δÃ 밁 Š 밁 QY BASE COUNT ORIGIN FEATURES Š 밁 밁 뭥 δÃ 밁 ρy Š 밁 Š Query Match Best Local S Matches 460 46191 46131 CTTGGGAATCTAAGAAGCTTCACATTCAGAGAACTCCATGTTTATACAGATGGTTTCAGT 46431 46371 46311 TTTCGTATGGAGCTAGAGATGATTAGCTTAGCTGTTCATAAGAATCTGCTTCGGTTAATT 46251 1027 source 967 907 847 cttggtcaactgaagaggttttctctgcgagaattgcaagtcgcaacggatacttttagt TCCAAGAACATTCTCGGCGCTGGTGGATTCGGTAATGTGTACAGAGGCAAGCTTGGAGAT GGTTATTGCGCAACTTCTGGTGAAAGGCTTCTTGTTTACCCCTTACATGCCTAATGGAAGC 46430 ggtttctgcatgacaccaacagagcggcttcttgtatatccatacatggctaatggaagt 1026 tttcaaacagaggtggaaatgattagcatggctgtgcatcgaaatcttctgcgtctacgt 966 GGGACAATGGTGGCAGTGAAACGGTTGAAGGATATTAATGGAACCTCAGGGGATTCACAG aggctgttgtaggtgattttgggttagctaggctcatggattacaaggatacccatgtta atcccaagattatccatcgtgatgtaaaagctgcaaatatattattggacgaagaatttg TGAGGAAGAGGATAGCAATTGGTGCAGCGAGAGGTTTGTTGTATCTACATGAGCAATGTG ctaggaagaggattgcactaggatctgctagggggctttcttatttgcatgaccattgtg 1141 CGATGAGTTTTAACCAATTTTGTTTAACTGTTGTAGCTAAACCGGCATTGGACTGGAACA GTCGCCTCTAAGCTTAAATGTTAGTATAATGTCTTGAACCATCAGTCCAAATCTCATTTT gttgcgtc-----ATCCCAAGATCATTCATAGAGATGTAAAGGCAGCTAATATTCTCTTAGACGAGTGCTTTG al Similarity 460; Conserv Actual end is 43094 Conservative start of this clone at 134784 of F17123. /organism="Arabidopsis t /cultivar="Columbia" /db_xref="taxon:3702" /clone="F17I23" /chomosome="IV" /map="unknown" a 23410 c 23696 g 4458 Location/Qualifiers .134784 11.9%; gtgtttaagagagcgtcagccatcag------0 Score 216.2; DB 8; Pred. No. 2.2e-38; 0; Mismatches 238; ŝ at base **,**+ -aacctccccttgattggccaa 1081 position Length 134784; Indels of. 71; F17I23; Gaps 1061 906 46190 46550 46370 46250 1201 46310 46490 46670 46610 actual ω

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Unpublished (1997)
2 (bases 1 to 120787)
2 (bases 1 to 120787)
Federspiel,N.A., Davis,R.W., Conway,A.B., Palm,C.J., Conway,A.R., Kurtz,D.B., Buehler,E., Dewar,K., Feng,J., Kim,G., Li,Y., Shinn,P., Sun,H., Oji,O., Osborne,B., Shen,Y.K., Toriumi,M., Vyotskaia,V., Direct submission.
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Submitted (09-UUL-1997) Biochemistry, Stanford University/DNA
Sequencing and Technology Center, 855 California Avenue, Palo
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Federspiel,N.A., Palm,C.J., Conway,A.B., Kurtz,D.B., Conway,A.R., Rederspiel,N.A., Brendel,V., Buehler,E., Dewar,K., Feng,J., Rim,C., Li,Y., Oji,O., Osborne,B.I., Shinn,P., Sun,H., Toriumi,M., Yyotskaia,V., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
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                                                                                         Submitted (11-JUL-1997) Biochemistry, Sequencing and Technology Center, 855
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Au,M., Araujo,R., Brendel,V., Buehler,E., Dewar,K., Feng,J.,
Kim,C., Li,Y., Oji,O., Osborne,B.I., Shinn,P., Sun,H., Toriumi,M.,
Vyotskaia,V., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
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Conway, A.B.,
                                                                                         Stanford University/DNA California Avenue, Palo Alto
Kurtz,D
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Oji,O., Osborne,B.I., Shim,P., Sun,B., Torlumi,M.,
Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S C
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Jul 11, 19
                                                                                                                                                                         /protein_id="AAB71970.1"
/db_xref="01:2462751"
/db_xref="01:246275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYFDNFLPSPVPHLALSALKKIDWKKYGLILANVNDQDGHVFLEWDNFPSYVQIQIAL
HWYHNQYPTRQKNGFGISLLKKGIKNALDNLKAKHBGFLLSHISKICGYVPDLARSI
AGLIFSSTDLDFQGDCLSVLGFQTQEVERDTVENYIGKILTYHIGMNERKPQKDQEAA
PFLFFDGESETSFFEDEEVEDENSTHEYDATATKAYTQFKCLATMLQE*
COMPLEMENT;3171...4444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="F8A5.1"
join(177. .214,632. .707,1132.
1845. .2159,2256. .2526,2788. .
/gene="F8A5.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAB71954.1"
/db_xref="GI:2462735"
/db_xref="GI:2462735"
/translation="MCCRWYTLRQNDFGTEVSLSVEGSMDVLVAPIIGFFQKIIVLQI
LNYTLDLAWKQGTSGRAQCYYFAVNADKTPCETASNLERLKSGLEDYVLRHANCLDT
MCDYCFSDREHLKYGSGTYCQEDKHKRYGGTMEYVIVISDLLESTQHCSRSCNGKTEV
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/translation="MGANEFRFFLSCDINSPVTFRIEKLDGNLPVKKSSDSGVVSIAE
EKKPELYIECALYIDGAPFGLPMRTRLKTTGPPYCWNELITLSSKYRDLTAHSQLAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (9782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNNIANKVSTF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative ADP-ribolylation factor"
/protein_id="AAB71955.1"
/protein_id="AAB71955.1"
/db_xref="G1:2462736"
/translation="MGI.SFAKLFSRLFAKKEMRILMVGLDAAGKTTILYKLKLGBIDE
/translation="MGI.SFAKLFSRLFAKKEMRILMVGLDAAGKTTILYKLKLGBIDE
LRDAVLLVFANKQDLPNAMNAAEITDKLGLHSLRQRHWYIQITCATTGEGLYEGLDWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(8347. .8443,8539.
/gene="F8A5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(8347. .9066)
/gene="F8A5.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="F8A5.2"
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/db_xref="taxon:3702"
/chromosome="I"
177. .2876
                                                     /product="Phosphatidylinositol 3-kinase"
/protein_id="AAB71971.1"
/db_xref="GI:2462752"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="nearly identical to rice protein gp|D26537|537404"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="F8A5.4
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                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                       'note="AtVps34"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'codon_start≠1
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.2876)
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.11164,11286.
.12395,12475.
.13572,13659.
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VWDVSCGKTEGLIGGATVLLENSKMONKSGKOKLRLWOGKEADGSFPTSTPGKVPRHE
RGELERLEKLMNKYERGOJOSIDWIDBLMLKSLDTIREDGESTKEGSSHLFVVVDFCCSF
EHRVVFQESGANLFITAPIGSTNEFVTVWDTELGKTNPSENKOLKLARSLDRGIIDRD
LKPSNIERKSIORYLKKYPFTRTISGDERQLLWEIFESLMSEKRALIKFLRCVWSDVO
EAKQAIQLMYKWEMIDVCDALELLSPLFESESVRAYAVSVLERADDEELGCYLLOLVO
ALRFERSDRSCLSGFLVORALQNIELASFLRWYVAVELHDHVYAKRFYSTYELLEENI
IKLPFOYNGEDGYQLWGSLVGOTETAGLCSITTREVRAVRGNTOKIEKLAQLIGGLL
SELTYFEEPIRSPLTPMYLIKGIVAGESSLFKSALHDLRIFFRFPEEGGSCKLIFKKG
DDLRQDGLVVQMVWLMDRILKLENLDLCLIFPYKVLATGHDEGMLEFIPSRSLAGIISE
HRSITSYLQKFERDEHAPFGITATCLDFFIKSCAUSVITYILGIGDRHLDNILLITDD
GRLFHYDFAFILGRDRRFFPPPMKLCKEMVELMGGAESGYTTREKSYCCEAYNILRKS
SNLILNLFHLMAGSTIPDIASDPEKGILKLQEKFRLDMDDEACHFFQDLINESVSAL
FPQMVETHRWAYDAYM*

15572. . . 17812
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/PICTEAL_16-"ABB71956.1"
/PICTEAL_16-"ABB71956.1"
/PICTEAL_16-"ABB71956.1"
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IRPLLDTVDLKRLNVKREGIQLFITVVVGDQSSGKSSVLDSLAGISLPRQGGICTRV
PLVMRLQRSSSPVPEIMLEYSDKIVPTDEEHLAEALGAATDVILAGWGPISYHGRSSRY
NSRPVNGQPENIYEQISGMIMKYIEPQESIILAVLSAIKPHWRRAYEQARAQEELLFR
YHPMLSLIDEDIVGIPVIAQKLMLIQARMISRCLPETYRKIHHKMETAVLELMKLPMV
ASTGEALMALMDIIGSAKESLFRILVGGDFSEPDDQMHCTARLADMLSQFSDNLQ
EKPKEVTEFLMNEIKIILDECKCVGLPNFIPRSAFLAILSVEHVLEIVEMEKLTDYTCM
YIEVVLSSVIAAYSENFPQIGSAIKRAGRNLIIKIKEHSVEKVLEIVEMEKLTDYTCM
PEYMTSWTOMTAEQQNEIYAULSDGKKPEHFSLTGFGGIVKISHTRKYHAHLLQAFD
PEYMTSWTOMTAEQQNEIYAULSDGKKPEHFSLTGFGGIVKISHTRKYHAHLLQAFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /traisiation="mykkvatkknspslaiakkksrsnkdvvsveapiissyndrir
PLLDTVDRLRNLNVMREGIHLPTIVVVGDQSSGKSSVLESLAGISLPRGQGICTRVPL
VMRLQSSSPEPEIWLEYNDKVVPTDEEHIAEAIRAATDVIAGSGKGVSDAPLYLEVK
KAGVPDLTMVDLPGITRVPVNGQPENIYEQISGMIMEXIEPQESIILNVLSATVDFTT
CESIEMSRKVDKTGQRETLAVVTXADMAPEGLLAKVTADDVSIVLGYVCVRNRIGEETY
EEARMQEELLFRTHPVLSLIDEDIVGIPVLAQKLMLIQSSMIARCLPKIVSKINQKLD
TAVLELNKLPMVMASTGEALMALMDIIGSAKESLLRILVQGDFSEYDDQNMRCTARL
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join(15572. .16004,16236. .17812)
/gene="F8A5.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21973. .22091,22335. .22510)
/gene="F885.6"
/note="similar to "Mx" GTP-binding
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="F8A5.6"

join(18712. .19150,19685. .1

21973. .22091,22335. .22510)

/gene="F8A5.6"
                                                                                                                                                                         VPDLTMVDLPGITRVPVNGQPENIYEQISRMINKYIEPQESIILNVLSATVDFTTCES
IRMSRQVDKTGERTLAVVTKADMAPEGLLQKVTADDVSIGLGYICVRNRIGEETYEEA
RVQEDLLFRTHPLLSLIDGDIYGIL"
                                                                                                                                                                                                                                                                                /translation="mggskmsndyeidveagmsslsivntpieapivssyndrirpll
DTVDRLRNLNVMREGIQLPTIVVVGDQSSGKSSVLESLAGINLPRGQGICTRVPLVMR
LQRSSSPEPEIMLEYSDKVVPTDEEHVAEAICAATDVIAGTGEGVSDTPLTLSVKKNN
                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/protein_id="AAB71957.1"
/db_xref="GI:2462738"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="F8A5.7"
join(23787..24210,24676.
/gene="F8A5.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYTPLTLHVKKADVPDLTLVDLPEITRVPVNGQTQNIHAKNLQGDYEVHQAT
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KDAVAAIVDQSSGELLALSLKSGLSTITEELILMSDEEHIAEAISSAAEAIAGSGKGV
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/db_xref="GI:2462747"
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                                                                  complement(join(26476. .26936,27030. .28070,28540.
                                                                                                      complement(26476. .28975)
/gene="F8A5.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to "Mx" GTP
11.9%;
Score 215.4;
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BB
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8;
Length 120787
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                                                                                         KEYWORDS
                                                                                                                                                               DEFINITION
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                                                                                                              VERSION
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                                                       ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGGGATTGTGTACAAAGGACACTTAAACGATGGAACTTTGGTGGCTGTCAAACGTCTCA 108913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ttggtaaggtgtataagggacgccttgctgatggctcacttgtagcagttaaaaggctta 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gagaattgcaagtcgcaacggatacttt-----tagtaccatacttggaagaggtggat 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTTTGCAGAACAATATGATCCAGAAGTGAGTTTAGGGCCACTTGAAGAGGTATACATTCA 109033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aagaagaacgaacaccaggtggtgagctgcagtttcaaacagaggtggaaatgattagca 934
                                                                                                                                                                                                                                                                                                     cttttgatcttgctcgccttgcgaacgatgatgatgttatgtt 1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agattatccatcgtgatgtaaaagctgcaaaatatattattggacgaagaatttgaggctg 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agaggattgcactaggatctgctagggggctttcttatttgcatgaccattgtgatccca 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ttcttgtatatccatacatggctaatggaagtgttgcgtcgtgtttaagagggcgtcagc 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tggctgtgcatcgaaatcttctgcgtctacgtggtttctgcatgacaccaacagagcggc 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTTGATTTTGGCAGATCCGCACACCAGAAAGGTGTAATGCT 108270
                                                                                                                                                                                                                                                                                                                                                                   agaagaccgatgtctttggttatgggattatgctcttagagctcattactggacagagag
                                                                                                                                                                                                                                                                                                                                                                                                                         CAGTCCGTGGAACTGTTGGCCACATTGCACCTGAGTACTTATCCACGGGTCAGTCCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                              ctgtaaggggtaccttgggctacatagctcccgagtacctctcgactggaaagtcatcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGTIGGTGATTITGGGTTAGCTAAGCTTCTAGACCATAGAGACTCTCATGTCACAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ttgtaggtgattttgggttagctaggctcatggattacaaggatacccatgttacaactg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTACATTTTTTGTTTAGATAATATCCGTGGAGAGCCAGCATTAGACTGGTCGAGAAGGA 108613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITTAGTCTACCCTTACATGCCAAATGGGAGTGTCGCATCACGCTTAAAAGGTAATGCAG 108733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGCTCTTCATCGCAATCTCCTCCGGCTCCGCGGTTTCTGTAGTAGCAACCAGGAGAGAA 108793
                                                                                                                                                                                                                                                                                                                                                  AGAAGACTGATGTCTTTGGCTTTGGCATACTTCTCCTTGAGCTCATTACTGGTCAGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGATTATACACCGCGATGTGAAAGCAGCTAACATTCTGTTAGATGAGGACTTCGAAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAAGATAGCGGTTGGGACAGCGAGAGGACTAGTTTACCTACACGAGCAATGTGACCCGA
                                                                                                                         AC005170
Arabidopsis thaliana Eukaryota; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                               AC005170 110211 bp
Arabidopsis thaliana
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                                                                        thale cress.
                                                                                                            sequence.
) AE002093
).2 GI:6598
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0; Mismatches 251;
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                                                                                                                                                                   II section
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                                   gene
                                                                                                                                                         repeat_region
                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ftp://arthur.gem.crn1.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 110211)
1 (bases 1 to 110211)
1 (bases 1 to 110211)
1 (lin, X., Kaul, S., Rounsley, S.D., Shea, T.P., Benito, M.-I., Town, C.D., Fulfil, C.Y., Mason, T.M., Bowman, C.L., Barnstead, M.E., Fulfil, C.Y., Mason, T.M., Rouning, C.M., Feldblyum, T.V., Buell, C.R., Ketchum, K.A., Lee, J.J., Rouning, C.M., Koo, H., Moffat, K.S., Cronin, L.A., Shen, M., Vanaken, S.E., Umayam, L., Tallon, L.J., Gill, J.E., Adams, M.D., Carrera, P.J., Crosasy, T.H., Goodman, H.M., Somerville, C.R., Copenhavera, P., Frenser, C.M., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (13-DEC-1999) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA. On Dec 17. 1999 this sequence version replaced gi:3738313. The sequence and annotation of chromosome 2 were merged from the individual clones on this chromosome after removing of the individual clones on this chromosome after removing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D., Nierman, W.C., White, O., Elsen, J.A., Salzberg, S.L., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genes were identified by a combination of three methods: Gene prediction programs including GRAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     overlaps. For detailed information, please see the TIGR web site (http://www.tlgr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rin,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 402 (6763), 761-768 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           We thank the CSHL/WashU/ABI consortium for sequencing BAC clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         numbered from the top to the bottom of the chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Energy and the US Department of Agriculture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This work was supported by the National Science Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          database support.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 all correspondence to:
                                                                                                                     /note="sequence from clone F27L4"
complement(356. 401)
/rpt_family="(TAA)n"
complement(join(1549. .2058,2731. .3012))
/gene*At2g/3810"
complement(1549. .3012)
/gene*At2g/23810"
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/db_xref="taxon:3702"
/chromosome="2"
                                                                                                                                                                                                                       complement(1. .2793)
                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                          location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        at@tigr.org
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                                       CDS
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complement(3570. .3641)
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complement(4565. .4612)
/rpt_family="(CAA)n"
6379. .6484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(6654. .6712)
/rpt_family="(GAA)n"
join(<9531. .9582,9709. .9779,9866.</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MKNUNRVFFCKSLSLVFLVPSFTRSHIRFTYSAAGASSPNAAIH
CMASDSPGSGDGSVSSPPNVAAVPSSSSSSASALDFLSLCTLKATPRAGWIKADV
KDPBSIADHMYRWGLMALISSDIPGVWRDKCWKMAIVHDLAEAIVGDIT$SGSIEKEDV
KDRESIADHMYRWGLMALISSDIPGVWRDKCWKMAIVHDLAEAIVGDIT$GSGIEKED
KNRRESEALEHMCKLLGGGERAKEIAELWREYEENSSPEAKVVKDFDKVELILQALEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(6480. .6749,7602. .
8152. .8268,8487. .8557)
/gene="nAt2g23820"
/note="unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="(CAAAA)n"
join(<6480. .6749,7602.
8152. .8268,8487. .8786)
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complement(3567. .3677)
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15853. .15918
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complement(11332...11371)
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IVFLVFLIIVYSVGCCAFRNNKRDDSYSRTYGYKP"
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10268. .10396)
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Best Local Similarity
Matches 467; Conserv
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VKASPAVTAKEVTLETFNKESGHLVEETKLRVTYVCSTTINITSPPRTRNGLYFNVFV
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GCAAGTCTGTTAGCCAGAAAGGAGCTATGCT 53535
              ctcgccttgcgaacgatgatgatgttatgtt 1430
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Search completed: June 23, 2000, 23:41:42 Job time: 43857 sec

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WPI; 98-086529/08.
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production of apomictic seeds - useful in plant breeding Claim 27; pages 91-95; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing
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Arabidopsis thaliana SERK receptor kinase; apomixis; plant breeding; ds.
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Matches 1191;
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Apomixis allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.

Seed and forage quality and maturity.

Sequence 2089 BP; 568 A; 419 C; 503 G; 599 T;
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aatcttctgcgtctacgtggtttctgcatgacaccaacagagcggcttcttgtatatcca
                          CCAGGTGGAGAGCTCCAGTTTCAAACAGAAGTAGAGATGATAAGTATGGCAGTTCATCGA
                                           | ccaggtggtgagctgcagtttcaaacagaggtggaaatgattagcattggctgtgcatcga
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3731. .3802
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                                       "contains
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Pr Production of apomictic seeds - useful in plant breeding
PS Claim 21; Pages 40-46; 123pp; English.

CC The sequence is that encoding SERK, a putative receptor kinase.

CC It may be used as part of a method of producing apomictic seeds

CC comprising: (a) transforming plant material with a nucleotide

CC comprising: (a) transforming plant material with a nucleotide

CC cell membrane renders the cell embryogenic; (b) regenerating

CC cell membry osc. The apomictic seeds and embryos thus produced

CC plant parts; and (c) expressing the sequence in the vicinity

CC of the embryo sac. The apomictic seeds and embryos thus produced

CC can be developed into plant progeny. This is useful in plant

CC threeding programs. Controllable and reproducible apomixis provides

CC many advantages in plant improvement and cultivar development in

CC the case that sexual plants are available as crosses with the

CC apomictic plant. Apomixis provides for true-breeding, seed

CC process so that selfing and progeny testing to produce and/or

CC stabilise a desirable gene combination could be eliminated.

CC specific stable traits for such characteristics as height,

CS seed and forage quality and maturity.

Sequence 6695 BP; 1844 A; 1182 C; 1243 G; 2422 T;
                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 735; Conserv
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20-NOV-1997; E02443.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
(NOVS ) NOVARTIS AG.
De Vries SC, Hecht VFG, Schmidt EDL, Van Holst WPI; 98-086529/08.
P-PSDB; W47013.
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/number= 6
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gttaaaagccttttgaaagagaaaaagttggagatgctggtcgatcctgacctggagaac
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                                                                                                     CCTTGCGAACGATGATGTTATGTTGGTTGGATTGGGTATGTGTCCCGGGTGTTCCTTT
                                                          ccacatcgaacttctgaatggatcctagactcgacagataacttgcatgcttttgaatta 1740
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                                               CCACATCGAACTTCTGAATGGATCCTAGACTCGACAGATAACTTGCATGCTTTTGAATTA
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03-AUG-1998 (first entry)
Arabidopsis thaliana SERK
Arabidopsis thaliana SERK
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Key
CDS
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plant breeding; ds.
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/number 4
4430. .4528
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3731. .3802
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Claim 26; Pages 64-67; 123pp; English.

The sequence is that encoding SERK, a purative receptor kinase.

It may be used as part of a method of producing apomictic seeds comprising; (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sc. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the propagated hybrids and could shorten and simplify the breeding process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated.

Apomixis allows plant breeders to develop cultivars with seed and forage quality and maturity.

Sequence 4081 BP; 1120 A; 770 C; 785 G; 1406 T;
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Best Local S
Matches 504
 3602
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Pred. No. 7.
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2772 CAGTAAAGCGACTTGCTGTAGGACGTTTTCAGGGGATT----CAACAGTTTGATGCAGAAA 2828

cagttaaaacgcttaaagaagaacgaacaccaggtggtgagctgcagtttcaaacagagg TAGGCAGTGGAGGTTTTGGAGCAACATACAAAGCGGAGATTGCACCAGGGTTCCTAGTGG ttggaagaggtggatttggtaaggtgtataagggacgccttgctgatggctcacttgtag

Query Match Best Local S Matches 350

Similarity

7.9%;

Score 143.4; DB 1; Pred. No. 3.2e-27; 0; Mismatches 296;

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Length

3842;

9

Gaps

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2771

Conservative

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                                                 New RRK polynucleotides and nucleic acid constructs - used for generating transgenic plants resistant to Xanthomonas Claim 14, Page 61-62, 67pp; English.
This invention describes a method for conferring disease resistants invention describes the use of novel genes and prote plants. The invention describes the use of novel genes and prote belonging to the Oryza longistaminata and Oryza sativa receptor kinase-like protein (RRK) Xa21 multigene family. Such genes from cassava, maize and tomato are also described. The genes and protesses the cassava, maize and tomato are also described. The genes and protesses the cassava, maize and tomato are also described.
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 be used for enhancing resistance to Xanthomonas in rice or tomato.

Sequence 3842 BP; 984 A; 719 C; 894 G;
                                                                                                                                                                                                 Wang G;
WPI; 99-204431/17.
P-PSDB; W23533.
                                                                                                                                                                                                                                                                                                                                                                              17-JUN-1999 (first entry)
Tomato Xa21 clone TRK2 DNA fragment.

Xa21; receptor kinase-like protein; multigene family; RRK; ric
Ya21; receptor kinase-like protein; multigene family; RRK; ric
Plant disease resistance; cassava; maize; tomato; Xanthomonas;
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X23533;
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13-AUG-1997; US-910386.
(REGC ) UNIV CALIFORNIA.
Hulbert SH, Richter T, Ronald
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                                    a plant,
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preferably in
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         New receptor kinase Bin1 involved in brassinolide signalling useful for promoting increased yield and disease resistance in plants and for modulating oocyte maturation

T plants and for modulating oocyte maturation

S Claim 8; Page 49-52; 72pp; English.

In this DNA sequence codes for a novel plant steroid receptor kinase, the synthesis of the plant steroid hormone, brassinolide. 18 New C arabidopsis dwarf mutants were identified that lacked the ability to respond to brassinolide, and were named bin mutants. The bin1 mutations were used to map the gene to a small interval on Arabidopsis chromosome 4. Bin1 was cloned by map-based cloning. The Bin1 polynucleotide was identified within this interval by sequencing the wild-type and mutant alleles of this nucleic acid.

Overexpression of Bin1 in transgenic plants provides plants
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30-DEC-1998.
24-JUN-1998: U13100.
24-JUN-1997: US-881706.
(SALK ) SALK INST BIOLOGICAL S:
Chory J, L1 J;
WPI: 99-081275/07.
P-PSDB: W97819.
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Arabidopsis steroid receptor Binl DNA.
BIN1; steroid receptor; receptor kinas
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Best Local Similarity 53.6
Matches 343; Conservative
17-JUN-1999 (first entry)
Maize Xa21 gene DT4 cDNA fragment.
Xa21; receptor kinase-like protein;
plant disease resistance; cassava; n
Zea mays.
Wo9909151-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plant yield or vegetative biomass and increased seed yield. Expression of Bin1 may also increase resistance to pesticides. Inhibition of Bin1, e.g. using antisense oligonucleotides (AON), is used to render plants male-sterile, and to reduce their stature or yield, e.g. for creating dwarf varieties. Since Bin1 homologues may be involved in regulation of the menstrual cycle and uterine function, Bin1, antibodies and AON may be useful as contraceptives, for improving success of in vitro fertilisation and to prevent premature labour. Transgenic animals are also provided, and are models for studying steroid-receptor interactions or can be used to screen for therapeutic agents.

Sequence 4104 BP; 1061 A; 870 C; 930 G; 1243 T;
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                                    tomato;
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Best Local Similarity
Matches 336; Conserv
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17-JUL-1998; U14841.
13-AUG-1997; US-910386.
(REGC ) UNIV CALIFORNIA.
Hulbert SH, Richter T, Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New RRK polynucleotides and nucleic acid constructs - used for generating transgenic plants resistant to Xanthomonas claim 12; Page 58-59; 67pp; English.

This invention describes a method for conferring disease resistance in plants. The invention describes the use of novel genes and proteins belonging to the Oryza longistaminata and Oryza sativa receptor kinase-like protein (RRK) Xa21 multigene family. Such genes and proteins canssava, maize and tomato are also described. The genes and proteins can be used for enhancing resistance to Xanthomonas in a plant, preferably in
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WPI; 99
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Sequence 3045 BP;
             T31307 standard;
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                                                                                  CGACTGAATTCGGCGACAATAAT
                                                                                                                                                                                             GAACACCTGGTTATGTGGCTCCCGAGTACTTCCAGTCGGTTATTTGCACAACTAAGGGCG
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                                                                                                                                                                                                                                                                          ttgggttagctaggctcatggattacaaggatacccatgttaca---actgctgtaaggg
                                                                                                                                                                                                                                                                                                        GGGACATGAAGTCAAGCAACGTGCTTCTTGACGATAATCTCGATGCCTACGTATCGGATT
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                                                                                                                                      Conservative
              cDNA; 1554
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              ВP
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Pred. No. 6.6e-27;
D; Mismatches 281
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CDNA clones TRK1 (T31307) and TRL1 (T31308) were isolated from the country of tomato conditions of the RRK conditions of tomato conditions of the RRK conditions of disease resistance genes. TRK1 (tomato receptor kinase 1) is present as 1 or 2 copies in the tomato genome and 1 copy maps to the short arm of chromosome 1 in the proximity of a resistance gene to Xanthomonas campestris pv. vesicatoria RX1. It encodes an RKK contradiction pathways leading to a defence response. The gene is consecuted for engineering disease resistance in tomato and other plants. So sequence 1554 BP; 477 A; 303 C; 348 G; 426 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 423
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17-JAN-1995; US-373374.
17-JAN-1995; US-475891.
07-JUN-1995; US-475891.
29-SEP-1995; US-004645.
(REGC ) UNIV CALLFORNIA.
Ronald PC, Song W, Szab
WPI; 96-354532/35.
P-PSDB; W03186.
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Tomato RRK gene clone TRK1.
Xa21; RRK; disease resistance; Xanthomonas; blight; rice;
Xa21; rrk; transgenic plant; crop protection;
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ATTGCAGGATCTTATGGCTACATTGCTCCAGAATATGCATACACGCTGAAAATTGATGAG
                                                                      GCAGATTTTGGATTAGCCAAGTACTTTCGTAACAATGGTACCTCTGAGTGCATGTCTGCA
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                                  gtaaggggtaccttgggctacatagctcccgagtacctctcgactggaaagtcatcagag
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Pred. No. 1.6e
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.6e-26;
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Best Local S
Matches 423
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17-JUL-1998; U14841.
13-AUG-1997; US-910386.
(REGC ) UNIV CALIFORNIA.
Hulbert SH, Richter T, Ro
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rice or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tomato Xa21 clone TRK1 DNA fragment.
Xa21; receptor kinase-like protein; multigene
plant disease resistance; cassava; maize; toma
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                                                                                                                                                                                                                                                                                                                                                                                              plants. The invention describes the use of novel genes and proteins belonging to the Oryza longistaminata and Oryza sativa receptor kinase-ilke protein (RRK) Xa21 multigene family. Such genes from cassava, maize and tomato are also described. The genes and protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        generating transgenic plants resistant
Claim 14; Page 59-60; 67pp; English.
This invention describes a method for o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lycopersicon esculentum. WO9909151-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New
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                                                                                                                                                                                                                                 793 accatacttggaagaggtggatttggtaaggtgtataagggacgccttgctgatggctca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRK polynucleotides and nucleic acid constructs - 
arating transgenic plants resistant to Xanthomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aagaccgatgtctttggttatgggattatgctcttagagctcattactggacagagagct
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                                                                                                                                                   CATGTCGCGGTGAAGAATTGGGAATAAGCAAAGGCTCACATGATAACGGCCTATCT---
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tcgtgtttaagagagcgtcagccatcagaacctccccttgattggccaactaggaagagg
                                               tgcatgacaccaacagagcggcttcttgtatatccatacatggctaatggaagtgtttgcg
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                               TGTTCAAACAAGGAAGTCAACTTGCTAGTTTATGAGTACATGCTAAATGGAAGCTTAG--
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e 3293
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Pred. No. 2.2e-26;
0; Mismatches 375;
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                                            DNA encoding plant morphogenesis regulatory protein - useful yield plants with short stems or altered inflorescence Claim 1; Pages 6-10; 17pp; Japanese.

The present sequence encodes an Arabidopsis thaliana plant morphogenesis regulatory protein (MRP), which can be used to a plant with, e.g. short stems or altered inflorescence. The acts on a plant at a specific site for a specific period, and therefore be used to regulate extraneous gene expression in a plant. The MRP's cDNA or genomic DNA can be used to transform
                                                                                                                                                                                                                                                                                                       Z4-AUG-1995; JP-216187.

(MITS-) MITSUI GYOSAI SHOKUBUTSU
(CHIKY) ZH CHIKYU KANKYO SANGYO G
WPI; 97-206629/19.

P-PSDR HTTOPA
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 Query Match
Best Local Sin
Matches 321;
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26-SEP-1996; Z54945.

26-SEP-1996; JP-254945.

(SAIS-) SAISHU JITSUYO G

WPI; 98-289869/26.

P-PSDB; W56307.
                                                                                  S-locus glycoprotein gene - and S receptor kinase gene of c
type and class II type to produce recombinant plants
Disclosure; Fig 2; 20pp; Japanese
The present sequence represents a class I S-receptor kinase
gene. The sequence was isolated from Brassica cammestris S45
Sequence 2640 BP; 800 A; 491 C; 645 G; 704 T;
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Clas I S-receptor kinase (SRK) c
Class I S-receptor kinase; SRK;
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Nasrallah JB, Nasrallah ME, (
PP-SDB; R99814.
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S-receptor; kinase; SRK; pistil; anther; stigmatic; self-incompatibility; primary; transmitter; pollen: signal; S-locus; binding domain; transmembrane; proglycoprotein; SLG; SRK6; SRK2; ZMPK1; ss.
New Brassica gene for S-receptor kinase, used incompatibility to plants - has extracellular to S-locus glyco-protein gene Claim 8; Page 51-52; 81pp; English.
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Best Local S
Matches 317
                                                                                                        SRK-AlO cDNA.

Slocus receptor kinase; SRK-AlO; S locus receptor kinase; SRK-AlO; S self-incompatibility; hybrid seed; self-incompatibility; hybrid seed; canola; oilseed; vector; ds.
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                                                                                    Brassica
Key
cds
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T13425;
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Pred. No. 4.1e-20;
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12-SEP-1995.
17-MAY-1994; 123751.
11-MAY-1994; US-208909.
11-MAY-1994; US-242104.
(ROTH/) ROTHSTEIN S J.
Glavin TL, Goring DR, J.
WPI; 96-180298/19.
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CDNA clone SRK-ALO (T13425) codes for an S locus receptor kinase associated with the ALO self-incompatability allele of Brassica napus. It was isolated from genomic DNA of rapeseed line WI by PCR amplification. The gene contains a 1 bp deletion resulting premature termination of translation and prodn. of truncated SRK protein. Expression vectors contg. a corrected SRK-ALO gene (se produce hybrid seed in improved yields. Sequence 2685 Bp; 816 A; 512 C; 639 G; 718 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1624
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                                                                                                                                                                                                                                                                                                                                                                      1978
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                                   gaagaccgatgtctttggttatgggattatgctcttagagctcattactggacagaga
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Pred. No. 5.7e
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11-MAY-1994; US-242104.
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S locus receptor kinase; SRK-A10; self-incompatibility; hybrid seed;
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PR (CHIK-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.

PA (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYU.

PA (CHIK-) ZH CHIKTU KANKYO SANGYO GIJITSU KENKYU.

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PCT-US-3-06251-83
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US-08-566-271-4
US-08-666-271-4
US-08-666-271-7
PCT-US-3-06251-7
PCT-US-3-07-44-1
PCT-US-3-07-47-1
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US-08-08-261-432-1
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US-07-717-331F-1

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US-08-447-185-2

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Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 14, Appl		Sequence 22, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 52, Appl	Sequence 51, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 7, Appli

ALIGNMENTS

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US-08-597-680A-24

Sequence 24, Application US/08587680A

Patent No. 5977434

GENERAL INFORMATION:

APPLICANT: Wang, Guo-Liang
APPLICANT: Wang, Guo-Liang
APPLICANT: Scabo, Veronique
TITIE OF INVENTION: Disease Resistance in Plants
TOTIES OF INVENTION: Disease Resistance in Plants
CORRESPONDENCE ADDRESS:

CORRESPONDENCE TOWNSEND And Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TIPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-TOS/MS-POS
SOFTWARE: Patenth Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
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APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/475,375
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/567,375
FILING DATE: 00-DEC-1995
PRIOR APPLICATION NUMBER: US 08/567,375
FILING DATE: 01-DEC-1995
PRIOR APPLICATION NUMBER: US 08/567,375
FILING DATE: 01-DEC-1995
PRIOR APPLICATION NUMBER: US 08/567,375
FILING DATE: 03-DEC-1995
PRIOR APPLICATION NUMBER: US 08/567,375
FILING DATE: 04-DEC-1995
PRIOR APPLICATION NUMBER: US 08/567,375
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RESULT 2
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                                                                                                               gagcggcctaagatgtcagaggtagtccgaatgctt 1605
                                                                                                                                                                                    gacacagaagttgagcagcttattcaagtagcattactctgtacccagggttcgccaatg
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                                                                                                                                                                                                                      TGGAGCAAAGAAGGGGTGGTGAAAATCTTGG-----ATGAGAGGCTAAAAAATGTTGCA
                                                                                                                                                                                                                                                                            GTAGGAAATTTTGGAGAAGGAATGGACATTGTACAATGGGCGAAAACGGAGACAAAA 1365
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ilarity 51.8%;
Conservative
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Pred. No. 4.2e-29;
0; Mismatches 375
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Best Local S
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-07-717-331F-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/07/717
FILING DATE: June 19th 1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
TELECOMUNICATION INFORMATION:
TELEPAX: (203)268-1951
TELEPAX: (203)268-1951
INFORMATION FOR SEQ. ID NO: 9:
INFORMATION FOR SEQ. ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua APPLICANT: Stein TITLE OF INVENTION: A Receptor Protein Kinase Gene TITLE OF INVENTION: Encoded At The Self-Incompatability Locus NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CITY: Trumbul
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                                                                                                                                              ttatccatcgtgatgtaaaagctgcaaatatattattggacgaagaatttgaggctgttg 1210
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                                                                                                                                                                                                                                                                                                                                                                          cgtcgtgtttaagagagcgtcagccatcagaacctccccttgattggccaactaggaaga 1090
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TCTCGGATTTTGGGATGGCCAGGATATTTGAAAGGGACGAAACGGAAGCTAACACAATGA
                                   taggtgattttgggttagctaggctcatggattacaaggatacccatgtt---acaactg 1267
                                                                                                          TAATCCACAGAGATTTGAAAGTAAGTAACATTTTGCTTGACAAAAATATGATCCCAAAGA
                                                                                                                                                                                                                                                                                                                                         ATTCTTATCTCTTTG---GTAAAACCCGAAGGTCTAAGCTAAATTGGAATGAGAGATTCG 1885
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTGCATTGAAGGAGATGAGAAGATGTTGATATATGAGTATTTGGAAAATTTAAGCCTTG
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US-07-717-331F-1
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Best Local Similarity
Matches 318; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/717
FILING DATE: June 19th 1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 26,824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
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1031 cgtcgtgtttaagaggggtcagccatcagaacctccccttgattggccaactaggaaga 1090
                                                                                                                                                                                                               1652 AAGAAATTGCAGTAAAAAGGCTATCAAAGACGTCAGTTCAAGGGACTGATG---AGTTTA 1708
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                                                                                                                                                                                                                                                                                                                   791 gtaccatacttggaagaggtggatttggtaaggtgtataagggacgccttgctgatggct 850
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CITY: Trumbull
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                                                           GTTGCATTGAAGGAGGATGAGAAGATGTTGATATATGAGTATTTGGAAAAATTTAAGCCTTG
                                                                                           totgcatgacaccaacagagcggcttcttgtatatccatacatggctaatggaagtgttg
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(203)268-1951
(203)268-1951
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                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Encoded At The Self-Incompatability Locus
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                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: POCHOPIEN Ph.D., Donald
REGISTRATION NUMBER: 32,167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-707-8889
TELEPHONE: 312-707-9155
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Rothst
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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CITY: Chicago
THATE: Illinois
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Goring, Daphne TITLE OF INVENTION: S-LOCUTION: SELF-
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                                                        ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                             MOLECULE TYPE: cD
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STRAIN: ol
INDIVIDUAL
                                                                                                                                                                      TYPE: nucleic acid
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APPLICATION NUMBER:
                                                                                                                                                       STRANDEDNESS: single
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                                       ORGANISM:
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                                                                                                                                                                   Sequence 2, Application US/08447185 Patent No. 5648599
GENERAL INFORMATION:
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Best Local Similarity
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NUMBER OF THE PROPERTY OF T
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AUTHORS: GORING, DAPHNE
AUTHORS: ROTHSTEIN, STEVEN J.
TITLE: THE S-LOCUS RECEPTOR KINASE GENE IN A
TITLE: SELF-INCOMPATIBLE BRASSICA NAPUS LINE
TITLE: FUNCTIONAL SERINE, THREONINE KINASE
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO
                                                                 APPLICANT: Tanksley, Steven D.
APPLICANT: MAITIN, Gregory B.
TITLE OF INVENTION: GENE CONFERRING DISEASE
TITLE OF INVENTION: TO PLANTS BY RESPONDING
NUMBER OF SEQUENCES: 5
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NAME: GOLDEN Mr., Michael L.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)263-1000
TELEPAX: (716)-263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
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Best Local Similarity
Matches 340; Conserv
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MEDIUM TYPE: Floppy
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OPERATING SYSTEM: PC-DOS/MS-DOS
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        tgggctacatagctcccgagtacctctcgactggaaagtcatcagagaagaccgatgtct 1342
                                                                                                                                                  TCAAGTCTATAAACATATTGCTTGATGAGAATTTTGTGCCAAAAATTACTGATTTTGGAA
                                                                                                                                                                       taaaagctgcaaatatattattggacgaagaatttgaggctgttgtaggtgattttgggt 1225
                                                                                                                                                                                                                                                                                                                 GATCAGATCTACCCACAATGAGCATGAGCTGGGGAGCAGAGGCTGGAGATATGCATAGGGG
                                                                      TATCCAAGAAAGGGACTGAGCTTGATCAAACCCATCTTAGCACAGTAGTGAAAGGAACTC
                                                                                           tagctaggctcatggattacaaggat---acccatgttacaactgctgtaaggggtacct 1282
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Pred. No. 4.1e-18;
0; Mismatches 299
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RESULT 6
US-08-447-185-3
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Goldman Mr., Michael L. TELECOMMUNICATION INFORMATION: TELEPHONE: (716)263-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION: 800
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tanksley, Steven D.
APPLICANT: Martin, Gregory B.
TITLE OF INVENTION: GENE CONFERRING DISEASE RESISTANCE
TITLE OF INVENTION: TO PLANTS BY RESPONDING TO AN AVIRULENCE GENE IN PLANT PATHOGI
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                               209
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986 cagagoggottottgtatatocoatacatggotaatggaagtgttgogtcgtgtttaagag 1045
                                                           326
                                                                                                                                      269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                       gaggtggatttggtaaggtgtataagggacgccttgctgatggctcacttgtagcagtta 865
                                                           CTCTCTCATTTTGCAGACATCCGCATCTGGTTTCATTGATAGGATTCTGTGATGAAAGAA 385
                                                                                                                                                                                                           ATGGTGTCTTTGGGAAGGTTTACAAGGGTGTTTTGCGTGATGGAGCAAAGGTGGCCCTGA
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                                                                                          tgattagcatggctgtgcatcgaaatcttctgcgtctacgtggtttctgcatgacaccaa 985
                                                                                                                                  AAAGGCGTACACCTGAGTCCTCACAAGGTATTGAAG---AGTTCGAAACAGAAATTGAGA
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                                                                                                                                                                                                                                                                                                                                                            Score 99.6; DB 1;
Pred. No. 6.7e-18;
0; Mismatches 299;
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US-07-717-331F-4
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                                                                                                                  US-07-717-331F-4
                                                                                                                                                                  TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2749 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/07717331F Patent No. 5484905
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GENERAL INFORMATION:
                                     Query Match
Best Local Similarity
                     Matches 305;
                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: GEOTGE M. Yahwak
REGISTRATION UNMBER: 26,824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/7
FILING DATE: June 19th 1991
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua APPLICANT: Stein
TITLE OF INVENTION: A Receptor Protein Kinase Gene
TITLE OF INVENTION: Encoded At The Self-Incompatability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1343
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                                                                                                                                  TOPOLOGY: 1
MOLECULE TYPE:
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                                                                                                                                                                                                                                           (203)268-1951
(203)268-1951
TD NO: 4:
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                     Conservative
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Encoded At The Self-Incompatability Locus
                                     5.1%;
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                     0
                 Score 92; DB 1;
Pred. No. 8.7e-16;
0; Mismatches 290
                                                       Length 2749
                   9
                 Gaps
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RESULT 8
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                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC COMS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Prote
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
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Suite 3400
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; LOCATION:
US-08-473-553A-1
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REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-60:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5733 base pairs
TYPE: nucleic acid
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                                                                                                                                                         sequence 3, Application Patent No. 5952485 GENERAL INFORMATION:
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Best Local :
                 APPLICANT: Ronald, Pameia C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 16
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CORRESPONDENCE ADDRESS:
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nes 232; Conserv
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5117..5467
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2434..5037
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51.3%;
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Pred. No. 2.1e-14;
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US-08-567-375-3
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Best Local Similarity
Matches 172; Conserv
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US 0
FILING DATE: 17-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 07-JUN-1995
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                                                                                   1364
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                                                                                                                                                                                                                                                         1244
                                                                                                                                                                                                                                                                                                                                                                                                                                   1126 ACTTCGCTTAGTTTTCTTGCACTTGAATTGAATAAGATCACAGGAAGCATTCCGAAGGAT 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                               1186 ATTGGCAATCTTATTGGCTTACAACATC--TCTATCTCTGCAACAACAATTTCAGAGGGT 1243
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1424 TGTCATTAGGCCTTTCAACTAATAACCTTAGTGGTCCAATACC 1466
                                                                                                                                                                                                              266
                                                                                                                                                                                                                                                                                                                                                                                 146 accttgacaaatatggggttcttatgacattggagctttacagcaataacataagtggac 205
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STREET: TW
CITY: San
                             386 aagtcctggatttatcaaacaatcggctatcaggaccagtacc 428
                                                                                                                                                                                                                                                                                       206 caattcctagtgatcttgggaatctgaccaatttggtgagcttggacctatacatgaata
                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 aattotatatgaatogtaacagtataaatatattaaattacatgcagttoactgatgctt 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: join(1..2676, 3520..3918)
OTHER INFORMATION: /product= "Xa-21"
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 29-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/004,645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                gcttctctggacctataccggacacattaggaaagcttacaaggctaagattcttgcgtc 325
                                                                                                                                                                                                                                                         CTCTTCCATCATCGTTGGGCAGGCTTAAAAACTTAGGCATTCTACTCGCCTACGAAAACA
                                                                                                                                                                     ACTTGAGCGGTTCGATCCCGTTGGCCATAGGAAATCTTACTGAACTTAATATCTTACTGC 1363
                                                                                   TCGGCACCAACAATTCAGTGGTTGGATACCATACACACTCTCAAACCTCACAAACTTGT 1423
                                                                                                                      tcaacaacaacagcctctctggtccaattccaatgtcactgactaatattacaactcttc 385
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Pred. No. 1.6e-06;
0; Mismatches 169;
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                                                                                                                                                   Query Match 3.2%;
Best Local Similarity 50.1%;
Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Ronald,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60,
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
APPLICATION NUMBER: US 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
1186 ATTGGCAATCTTATTGGCTTACAACATC--TCTATCTCTGCAACAACTTTCAGAGGGT 1243
                                                                          1126 ACTTCGCTTAGTTTTCTTGCACTTGAATTGAATAAGATCACAGGAAGCATTCCGAAGGAT 1185
                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IIILE OF INVENTION: Procedures and Materials for Conferring
IIILE OF INVENTION: Disease Resistance in Plants
                                    146
                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two Emparcac
CITY: San Francisco
                                                                                                 86 aattotatatgaatogtaacagtataaatatataaattacatgcagttcactgatgctt 145
                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bastian, Kevin REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08 FILING DATE: 17-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/01 FILING DATE: 17-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: California
                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: join(1..2676, 3520..3918)
OTHER INFORMATION: /product= "xa-21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                      accttgacaaatatggggttcttatgacattggagctttacagcaataacataagtggac 205
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                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                        3921 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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Song, Wen-Yuang
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                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                   single
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                                                                                                                                                   Score 58.6; DB 4;
Pred. No. 1.6e-06;
0; Mismatches 169
                                                                                                                                                                                           DB 4;
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US-08-475-891A-3
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,891A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BASTIAN, Keyin L.
NAME: BASTIAN, Keyin L.
                                                                                                                                                                                             TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5992 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
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APPLICANT: Ronald
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415,576,0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants
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                                                                                                                                                              MOLECULE TYPE:
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                                             OTHER INFORMATION:
OTHER INFORMATION:
                                                                                          NAME/KEY:
LOCATION:
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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    INFORMATION:
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Song, Wen-Yuang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ronald, Pamela C.
                                                                                                                                                     linear
E: DNA (genomic)
                                                                                            join(512..3149, 3993..4393)
/product= "RRK-B"
/note= "Xa21 Xanthomonas spp. disease resistance gene RRK-B from rice (Oryza sativa)"
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Query Match

3.28;

Score 58.6;

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Length 5992

Conservative

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Mismatches

Indels

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                                                                                                    TOPOLOGY: 11;
MOLECULE TYPE:
PCT-US93-06251-83
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Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 83, Application PC/TUS9306251 GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 122; Conserv
                                                                                                                                                                                                                                 TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: D1619110, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PATENTIA REFERENCE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
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TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1637 ACTTCGCTTAGTTTTCTTGCACTTGAATTGAATAAGATCACAGGAAGCATTCCGAAGGAT 1696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                 LENGTH: 4517 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 11530
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                                                                                                                           DNA (genomic)
                    3.2%;
                                                                                                                                                                                                                                                          83:
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                    Score 57.2; DB 6; Pred. No. 4.1e-06;
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Mismatches 169; Indels
                                        Length 4517;
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                                                                                                                                                                      ; NAME/KEY:
; LOCATION:
US-08-238-163-3
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Patent No. 5569830
GENERAL INFORMATION:
                                                                           Matches
                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1438
                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/00
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                      190 aataacataagtggaccaattcctagtgatcttgggaatctgacaaatttggtgagcttg 249
                                                                       Local Sinhes 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gctgtaaggggtaccttgggctacatagctcccgagtacctctcgactggaaagtcatca 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gttgtaggtgattttgggttagctaggctcatggattacaaggatacccatgttacaact 1266
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ACTAATCTCACCGGAACAATTCCACCTGCAATTGCGAAGCTCACAAATCTCAAAATGTTA 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSEE: Townsend and Townsend Khourie and Crew
T: Steuart Street Tower, One Market Plaza
San Francisco
: California
                                                                         h 3.0%;
Similarity 51.7%;
25; Conservative
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STOTZ, Henrik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LABAVITCH, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BENNETT, Alan
                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/238,163
                                                                       Score 54.8; DI
Pred. No. 1.2e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               2307E-540
                                                                       DB 1;
1.2e-05;
nes 117;
                                                                                                            Length 2075;
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US-08-475-891A-1
US-08-475-891A-1
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                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/373,375
ETILING DATE: 17-JAN-1995
ATTORNEY_AGENT LIFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34.774
REFERENCE_POCKET NUMBER: 02370-0589
TELECOMOUNICATION INFORMATION:
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APPLICANT: Ronald
                                                                                                                                                                                                                                                                               TELEFAX: (415) 576-030 INFORMATION FOR SEQ ID NO:
                                                                                                                                                               LENGTH: 6256 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
KOLFOFFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 06-JUN-: CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
          NAME/KEY: CDS
LOCATION: JOIN (1648
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                         FEATURE:
                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            430
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CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                        TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
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Song, Wen-Yuang
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                            join(1648..4383, 5178..5513)

WATION: /product= "RRK-F"

WATION: /note= "Xa21 Xanthomonas spp. disease

WATION: resistance gene RRK-F from rice (Oryza
                                                                                                                                                                                                                                                                                                (415) 576-0200
415) 576-0300
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                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Procedures and Materials for Conferring Disease Resistance in Plants
               sativa)"
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                                                                                                                                                                                                                                                                               1:
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Query Match

3.0%;

Score 53.8;

DB 3;

Length 6256;

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RESULT 15
US-08-567-375-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTMARE: Patentin Release #1.0, Ver CURRENT APPLICATION NUMBER: US/08/567,375 FILING DATE: 04-DEC-1995 CLASSIFICATION DATA: 800 PRIOR APPLICATION NUMBER: US 60/004,645 APPLICATION NUMBER: US 60/004,645 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/475,891 PRIOR APPLICATION DATA: US 08/373,375 PRIOR APPLICATION DATA: US 08/373,375 APPLICATION DATA: HAPPLICATION DATA: US 08/373,375 APPLICATION DATA: HAPPLICATION DATA: US 08/373,375 APPLICATION DATA: HAPPLICATION DATA: US 08/373,375 APPLICATION DATA: US 08/373,375 
                                                                                                                                                                                                                                                                                                  NAME: Bastian, Revin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-058930
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 576-0300
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
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APPLICANT: Ronald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
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                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
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TITLE OF INVENTION: Disease Resistance in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3065 ACACACTCTCAAACCTCACAA 3085
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                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 agctttacagcaataacataagtggaccaattcctagtgatcttggggaatctgacaaatt 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                            TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCTTACTGAACTTAATATCTTACTGCTCGGCACCAACAAATTCAGTGGTTGGATACCAT 3064
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; LOCATION: join(1648..4383, 5178..5513); OTHER INFORMATION: /product= "RRK-F"; OTHER INFORMATION: /note= "xa21 xantho); OTHER INFORMATION: resistance gene RRK; OTHER INFORMATION: (Oryza sativa)" US-08-567-375-1
Search completed: June 23, 2000, 22:42:10 Job time: 40076 sec
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/note-"ARK.F"
/note-"Ark.F from rice
resistance gene RRK-F from rice
(Oryza sativa)"
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Copyright (c) 1993 - 2000
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gb_gss14:
gb_gss15:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query

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JOURNAL
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COMMENT
                                                     REFERENCE
AUTHORS
TITLE
                                                                                                                                                          ACCESSION
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KEYWORDS
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AA738547
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 clones of
Mol. Gen.
98409267
On Nov 29
                                                                                                                                                          AA738547 656 bp mRNA EST 17-AUG-1998 SbRLK5 Sorghum bicolor cv. TX430 leaf Sorghum bicolor cDNA clc sbRLK5 similar to protein kinase, highest similarity to receptor-like protein kinases, mRNA sequence.
AA738547.1 GI:3421472 EST.
                                                                                                       sorghum.
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
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  version
 replaced
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AA736571 LÍLTNDEST
AA736571 BARCHIJON
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AA768670 EST012 SU
AA75217 8480 Lambda
AA73635 LILTNDEST
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AI967315 LJ1rnpest
AW042251 G14026B11
AO840411 nbxb0058F
AW224241 EST300968
C22490 C22490 R1ce
AI937984 sc06e07.y
AW201125 se98b06.y
AW2071213 nbxb00551
AI729170 BNLGH1128
g1:636097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggaagtgttgcgtcgtgtttaagagagcgtcagccatcagaacctccccttgattgg---
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                                                                                                                                   tgggttaaaagccttttgaaagagaaaaagttggagatgctggtcgatcctgacctggag 1497
                                                                                                                                                                        GGCCAGAGGGCATTTGATCTTGCTCGTCTTGCAAATGATGACGATGTTATGCTTCTTGAC 480
                                                                                                                                                                                     ggacagagagcttttgatcttgctcgccttgcgaacgatgatgatgttatgttgttggat 1437
                                                                                                                                                                                                                         GTCACAACTGCTGCGGGAACAATTGGACACATTGCGCCTGAGTACCTATCCACTGGC
                                                                                                                                                                                                                                                                                           gttacaactgctgtaaggggtaccttgggctacatagctcccgagtacctctcgactgga 1317
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                                                                                                                                                                                                                                                                                                                                                                                                    tgtgatcccaagattatccatcgtgatgtaaaagctgcaaatatattattggacgaagaa 1197
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               GGCTCCCCGTTGGACCTCCCAAAGATGTCGGAGGTGGTGAGGATGCTCGAAGGTGA
                                                                                                                    TGGGTGAAAGGACTGCTGAAGGAGAAGAAGGTGGAGATGCTGGTGGACCCAGATCTGCAG
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                                                                AACGCCTACGAGGAGCATCGAGGTGGAGAACCTGATCCAGGTGGCACTCCTCTGCACGCAG
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Institut fuer Entwicklungsbiologie und Molekularbiologie
Pflanzen.
Heinrich-Heine-Universitaet
Universitaetsstrasse 1, 40225 Duesseldorf, Germany
Tel: (49)-211-81-14871
Fax: (49)-211-81-14871
Email: stockha@uni-duesseldorf.de
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/dlone="SbRLK5"
/clone=Lib="Sorghum bicolor cv. TX430 leaf"
/clone_Lib="Sorghum bicolor cv. TX430 leaf"
/clone="green"
/dev_stage="green"
/note="Organ: leaf: Vector: Lambda ZAP II; Site_1:
Site_2: Xho I; leaf cDNA library from green leaves,
unidirectionally cloned"
unidirectionally cloned"
145 c 184 g 166 t
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/strain="cv. TX430"
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76.5%;
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Pred. No. 5.3
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Matches 599
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                                                                                                                            ttcaaacagaggtggaaatgattagcatggctgtgcatcgaaatcttctgcgtctacgtg
                                                                                                                                                                      GCACTAAGATTGCTGTAAAACGGTTAACTGATTACGAAAGTCCTGGTGGAGAGGCTGCTT
                                                                                                                                                                                        AGAAAAATGTTCTTGGACAAGGGGGCTTTGGGAAAGTATATAAAGGAGCACTTCCAGATG
ttgcgtcgtgtttaagagagggtcagccatcagaacctccccttgattggccaactagga
                                                               gtttctgcatgacaccaacagagcggcttcttgtatatccatacatggctaatggaagtg
                                                                                                                                                                                                                                                                                             TTGGCCAGTTGAAAAGATTTGCATGGAGAGAATTGCAACTTGCAACTGATAATTTCAGTG
                                             GTTTCTGTACAACACAAACAGAGCGCCTGCTTGTTTATCCTTTCATGCACAATCTTAGTG
                                                                                                          599;
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SbRLK2 Sorghum bicolor cv. TX430 leaf Sorghum bicolor cE
SbRLK2 similar to protein kinase, highest similarity to
receptor-like protein kinases, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Annen, F., Chang, J.-L.,
Characterization of 14
clones of the C4 plant
MO1. Gen. Genet. 259 (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Nov 29, 1993 this sequence version replaced Contact: Stockhaus J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Virice euphyllophytes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor-like
AA738544
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Fflanzen
Heinrich-Heine-Universitaet
Universitaetsstrasse 1, 40225 Duesseldorf, Germany
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(49)-211-81-14871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: leaf; Vector: Lambda ZAP II; Site_1: Eco
Site_2: Xho I; leaf cDNA library from green leaves,
unidirectionally cloned"
194 c 293 g 251 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Sorghum bicolor"
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| /db_xref="taxon:4558"
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| /clone_lib="Sorghum bicolor cv. TX430 leaf"
| /dev_stage="green"
| /dev_stage="green"
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Pred. No. 3.1e-7
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                                                                                                                              Shoemaker, R., Keim, P., Vodkin, L., Expelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                                Glycine max
Unpublished (1999)
On Feb 18, 1999 this sequence version rep
Contact: Shoemaker R/Public Soybean EST F
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 403.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2: /note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhOI; The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were innoculated with Bradyrhizobium japonicus, strain USDA110 priot to harvest. Stratagene's CDNA synthesis Kit (catalog number 200401) was used to synthesis the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's
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/clone_lib="Gm-c1028"
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/lab_host="DH10B"
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/db_xref="taxon:3847"
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Pred. No. 3.6e-75;
O; Mismatches 106;
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                             1325 cagagaagaccgatgtctttggttatgggattatgctcttagagctcattactggacaga 1384
                                                                                  1265 ctgctgtaaggggtaccttgggctacatagctcccgagtacctctcgactggaaagtcat 1324
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                                                               TACCTCTCAACTGGAAAGTCTTCAGAGAAGACTGATGTTTTTGGATATGGTGTGATGCTT
CAGAGAAAACTGATGTTTTTGGGTATGGTATCATGCTTTTTGGAGCTTATAACTGGACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gossypium hirsutum

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyliophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core

eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

1 (bases 1 to 555)

Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.

ESTs from developing cotton fiber
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AI728030 AI728030.1 GI:5046816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 516-344-3396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biology Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Jun 5, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: burr@bnlux1.bnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Ben Burr
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                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                 /organism="Gossypium hirsutum"
/cultivar="Acala Maxxa"
/db_xref="taxon:3635"
/clone_lib="Six-day Cotton fiber"
/tissue_type="immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="XLI-Blue"
/note="Yector: pBluescript II KS+"
/note="Yector: pBluescript II KS+"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                  19.4%;
77.5%;
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                                                                                                                                                                                                                    Score 352.6; DB 51; Length 555; Pred. No. 3.5e-73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA738545 1435 bp mRNA EST 17-AUG
SbRLK3 Sorghum bicolor cv. TX430 leaf Sorghum bicolor cI
SbRLK3 similar to protein kinase, highest similarity to
receptor-like protein kinases, mRNA sequence.
AA738545
AA738545.1 GI:3421470
EST.
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98409267
On Nov 29, 1993 this sequence version replaced
Contact: Stockhaus J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sorghum bicolor
                                                                                                                                                                                                                                                                 Heinrich-Heine-Universitaet
Universitaetsstrasse 1, 40225 Duesseldorf,
Tel: (49)-211-81-14953
Fax: (49)-211-81-14871
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                                                                                                                                                                                                                  Insert Length: 1900
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                                                                                                                                                                                                                                                 stockha@uni-duesseldorf
/dev_stage="green" /dev_stage="green" Vector: Lambda ZAP II; Site_1: /note="Organ: leaf; Vector: Lambda ZAP II; Site_1: Site_2: Xho I; leaf cDNA library from green leaves, unidirectionally cloned" a 300 c 389 g 381 t
                                                                                                /db_xref="taxon:4558"
/clone="SbRLK3"
/clone_lib="Sorghum bicolor
                                                                                                                                                  /organism="Sorghum bicolor"
/strain="cv. TX430"
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Pred. No. 2.6e-72;
0; Mismatches 300
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DEFINITION

AI900110 538 bp mRNA EST 06-DEC-1999 sc01a04.y1 Gm-c1012 Glycine max cDNA clone GENOME SYSTEMS CLO Gm-c1012-871 5' similar to TR:023921 023921 SOMATIC EMBRYOGEN

CLONE

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REFERENCE
AUTHORS
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                                1302
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                                                                                  \vdash
gtacctctcgactggaaagtcatcagagaagaccgatgtctttggttatgggattatgct
                                                                                     TTACAAGGACACGCATGTGACAACTGCTGTACGGGGCACTATCGGGGCATATAGCTCCTGA 60
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On Jun 5, 1998 this sequence version replaced 9
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECEPTOR-LIKE KINASE. ;, mRNA sequence. AI900110 AI900110.1 GI:5606012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
cail: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
Seq primer: -40Rp from Glbco
High quality sequence stop: 411.
Location/Qualifiers
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Shoemaker, R., Keim,
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae;
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314 286 1810
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XIIO-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolat from the apical shoots of 9 to 10 day old etholated seedlings. The shoot tips including any emerged leaves were harvested for mRNA isolation. The cDNA library was prepared using the Stratagene pBluescript II XR cDNA library construction kit. Complementary DNA was
                                                                                                                                                                                                                                                                                                                                                                   Erpelding."
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/db_xref="taxon:3847"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1012-871"
/clone_11b="Cm-c1012"
/clone_1tb="Cm-c1012"
/tissue_type="Apical shoot tips, 9-10 day old etiolated
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Shoemaker R/Public Soybean EST Project
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                                                                                                                                                                                                                      18.3%;
77.7%;
                                                                                                                                                                                           Score 332; DB 62;
Pred. No. 2.6e-68;
0; Mismatches 115
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EST265720 tomato callus,
cLEC14J5, mRNA sequence.
AI896277
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Clemson University
100 Jordan Hall, Clemson, SC 29634, U
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,
Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L.,
Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                          Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
On May 18, 1998 this sequence version replaced gi:3137451
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/tissue_type="callus"
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/dev_stage="25-40 days old"
/lab_host="xxl1-Blue MRF'"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
xho1; supplier: Giovannoni laboratory; cLEC - Cotyledons
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/cultivar="TA496"
                                                                                                                 /db_xref="taxon:4081"
/clone="cLEC14J5"
                                                                                                 /clone_lib="tomato callus,
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                        AI727837 597 bp mRNA EST 11-JUN-1999
BNLGH19209 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar
to (U93048) somatic embryogenesis receptor-like kinase [Daucus
Blewitt,M., Matz.E.C., Davy,D.F. and
ESTs from developing cotton fiber
Unpublished (1999)
On Jun 5, 1998 this sequence version
Contact: Ben Burr
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AI727837.1 GI:5046689
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        AA738546 655 bp mRNA EST SDRLK4 Sorghum bicolor cv. TX430 leaf Sorghum bicolor SDRLK4 similar to protein kinase, highest similarity receptor-like protein kinases, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 516-344-3396
Fax: 516-344-3407
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Seq primer: T3 Primer.
receptor-like
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/cultivar="Acala Maxxa"
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/tissue_type="immature fiber"
/dev_stage="Six days post anthesis"
/dev_stage="Six days post anthesis"
/lab_host="xil-Biue"
/note="Vector: pBluescript II KS+"
5 a 107 c 165 g 148 t 12 ot
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Local Similarity 65.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAAAGATTTGCATGGCGAGAATTGCAACTTGCAACTGATAATTTCAGTGAGAAAAATGT
tcgtgatgtaaaagctgcaaatatattattggacgaagaatttgaggctgttgtaggtga
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                                                                                             TATAGGCACAGCTCGTGGACTGGAGTATATGCACGAGCACTGCAATCCTAAGATTATACA
                                                                                                                                                                                                                                                                                                                                              AACACAAACAGAGCGCCTGCTTGTTTATCCTTTCATGCAGAATCTTAGTGTGGCCTACCG
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98409267
On Jan 13, 1998 this sequence version replaced gi:3421471.
Contact: Stockhaus J
Institut fuer Entwicklungsbiologie und Molekularbiologie d
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Annen, F. Chang, J.-L., Paterson, A.H. and Stockhaus, J.
Characterization of 14 different putative protein kinase clones of the C4 plant Sorghum bicolor
Mol. Gen. Genet. 259 (1), 115-122 (1998)
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Universitaetsstrasse 1, 40225 Duesseldorf,
Tel: (49)-211-81-14953
Fax: (49)-211-81-14871
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/clone="SbRLK4"
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/clone="SpRLK4"
/clone="Ib="Sorghum bicolor cv. TX430 leaf"
/clone="Ib="Sorghum bicolor cv. TX430 leaf"
/clone="SprLk4"

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Location/Qualifiers
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Pred. No. 3.1e-53;
0; Mismatches 213;
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Best Local :
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                                                                                                           ATGAACATTGCAATCCTAAGATCATTCATCGAGATGTGAAGGCTGCAAATGTATTATTGG 128
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                                     ATGAAGATTTTGAAGCAGTTGTCGGTGACTTTTGGCCTTGCGAAGTTGGTGGATGTGAGGC 188
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukhryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
On Jun 5, 1998 thi
Contact: Ben Burr
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1 (bases 1 to 703)
Blewitt,M., Matz,E.C., Davy,
ESTs from developing cotton
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Brookhaven National Laboratory
Upton, NY 11973, USA
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Fax: 516-344-3407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: burr@bnlux1.bnl.gov
                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                     188
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                      /organism="Gossypium hirsutum"
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/dev_stage="Six days post anthesis"
/lab_host="Xi-Blue"
/note="Vector: pBluescript II KS+"
note="Vector: pBluescript II KS+"
148 c 180 g 186 t 1 ot
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0; Mismatches
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5e-49;
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EST.
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EST244774 tomato ovary,
                                                                                                                                                                                                                                                                                Tel: 864 656 4366 Fax: 864 656 4293
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100 Jordan Hall, C
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   136
                                                                                                                                                                                                                                                              dfrisch@CLEMSON.EDU
                         /Clone_lib="tomato ovary, TAMU"
/tissue_type="carpel"
/tissue_type="carpel"
/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
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/lab_host="XL1-Blue MRF',"
/lab_host="XL1-Blue MRF',"
/lab_host="Tablue MRF',"
/lab_host="Library: ConfigodT-primed arthorized toward toward and carpel EST Library: OligodT-primed ardirectionally cloned cDNA in vector Lamda ZAP II with 5 directionally cloned at the EcoRI and XhoI sites,
                 respectively.
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/cultivar="TA496"
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A087p60u Hyb
tremuloides
                                                                                                                                                                                                                                                                                                             1 (bases 1 to 380)
Sterky, F., Regan, S., Karlsson, J., Hertzberg, M., Rohde, A.,
Holmberg, A., Amini, B., Bhalerao, R., Larsson, M., Villarroel, R.,
Montagu, M., Sandberg, G., Olsson, O., Teeri, T.T., Boerjan, W.,
Gustafsson, P., Uhlen, M., Sundberg, B. and Lundeberg, J.
Gene discovery in the wood-forming tissues of poplar: Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Populus tremula x Populus tremuloides.
Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eubhylicphytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
FORWARD: AAAGGGGGATGTGCTGCAAGGCGBACKWARD: GCTTCCGGCTCGTATGTTGTGT
                                                                                     Royal Institute of Technology (KTH)
Teknikringen 34, S-100 44 STOCKHOLM,
Tel: +46 8 790 8287
Fax: +46 8 24 54 52
                                                                                                                                                                               Contact: Sterky F
Department of Biotechnology
                                                                                                                                                                                                                          On Jan 17, 1998 this sequence
                                                                                                                                                                                                                                                                     5,692 expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 95 (22), 13330-13335 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI165643.1
                                                                  Email: fredrik@biochem.kth.se
                                               PCR PRimers
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Hybrid aspen plasmid library Populus tremula x Populus
des cDNA 5', mRNA sequence.
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Pred. No. 1.3e-42;
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REFERENCE
AUTHORS
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AW310334/c
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                                                                                                                                                                                                                                                                                                                   DEFINITION
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Best Local (
                                                                                                                                                                         ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gggttagctaggctcatggattacaaggatacccatgttacaactgctgtaaggggtacc 1281
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                                                                                                                                                                                                                                                                 AW310334 412 bp mRNA EST sf34f03.x1 Gm-c1028 Glycine max cDNA clone GE Gm-c1028-1878 3' similar to TR:023921 023921 RECEPTOR-LIKE KINASE. ; mRNA sequence.
                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
1 (bases 1 to 412)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Marti Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., A
                                                                                                                                                                                                              EST
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                                                                                                                                                                       Glycine max
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AW310334.1 GI:6725935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note "Vector: pBluescript SK; Site_1: SalI; Site_2: NotI. Cambial region tissues, including developing xylem, the meristematic cambial zone and the developing and mature phloem, was harvested from 1.5 m actively growing trees. cDNA was prepared and cloned into lambda gt22a. DNA was isolated and subcloned into pBluescript SK using SalI and NotI restriction enzymes."

a 67 c 99 g 102 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Populus tremula x Populus tremuloides"
/db_xref="taxon:47664"
/clone_lib="Hybrid aspen plasmid library"
/tissue_type="Cambial region"
/dev_stage="1.5 m actively growing tree"
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 43;
                                                                                                                                                                                                                                                                                           T 21-JAN-2000 EGENOME SYSTEMS CLONE ID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Theising, B., Allen, M.,
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                   Martin, J.,
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1240 gattaccaaggatacccatgttacaactgctgtaaggggtaccttgggctacatagctccc 1299

Conservative

0

Mismatches

129;

Indels

0

Gaps

0

353

293

1300 gagtacctctcgactggaaagtcatcagagaagaccgatgtctttggttatgggattatg 1359 412 GATCACACACATACTCATGTTACTACTGTTGTATNCCGTACGCCATGGCCAAATAGCACAC

GAGTTTCTCACAACTGAAAGGTCTTCAGAGAAGACTGATGTTTTTGGCATATGGCATCATG

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FEATURES
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Query Match

Best Local Similarity

Matches 278; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N. Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

McCann,R., Waterston,R. and Wilson,R.

McCann,R., Waterston,R. and Wilson,R.
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
On May 18, 1998 this sequence version replaced gi:3138263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4444 Forest Park Parkway, Box 8501,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shoemaker R/Public Soybean EST
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                                                                                                                                                                                                                      107
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314 286 1810
                                                                                                                                                                                                   first-strand synthesis primer was used. An 'anchor' nuclectide (V-A,C, or 6) was added to the 3 end of the primer [GAGAGAGAGAGAGAGAGAGTACTGCTCGAG(T)]8V] to anchor the primer [GAGAGAGAGAGAGAGACTAGTCTCGAG(T)]8V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their heatmethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) that has been digested with EcoRI and XhoI, and phosporylated by Stratagene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n-25). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were innoculated with Bradyrhizobium japonicus, strain USDA110 priot to harvest. Stratagene's CDNA synthesis Kit (Catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="roots of 'Supernod' plants"
/lab_host="DH10B"
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/db_xref="taxon:3847"
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                              11.1%; 68.3%;
                              Score 201.2; DB 7
Pred. No. 2.1e-37;
                                                                    DB 79;
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Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Rhanna,A., Bolla,B., Consoud,K., Steptoe,M., Theising,B., Allen,M.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
MCCann,R., Watterfor, P., A., William, D., Jackson,Y., Cardenas,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI416897 474 bp mRNA EST sal9e11.x1 Gm-c1005 Glycine max cDNA clone Gm-c1005-165 3' similar to TR:023921 023921
                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4
Parkway Circle St. Louis, Missouri 63134 For further ir
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-33
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
Possible reversed clone: Similarity on wrong strand
Seq primer: T7 ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                     Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, I Tel: 314 286 1810

Fax: 314 286 1810
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
On May 7, 1998 this sequence version replaced gi:3119924
Other_ESTs: saigeil.yl
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/clone="GENOME SYSTEMS CLONE ID: Gm-c1005-165"
/clone_lib="Gm-c1005"
/lab_host="XL10-Gold"
/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
XhoI; This library was constructed by Dr. Randy C.
Shoemaker and Dr. John Erpelding, USDA-ARS Agronomy
Department, G401 Agronomy Hall, Iowa State University,
                                                                                                                                  /organism="Glycine max"
/db_xref="taxon:3847"
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                     Tel: 864 656 4366
Fax: 864 656 4293
                                                          Clemson University
100 Jordan Hall, Clemson,
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       dfrisch@CLEMSON.EDU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW033961 524 bp mRNA EST 15-SEP-1999 EST277623 tomato callus, TAMU Lycopersicon esculentum cDNA clone CLEC3318 similar to A. thaliana putative serine/threonine protein
                         Generation of ESTs from tomato callus Unpublished (1999) on May 18, 1998 this sequence version Contact: David Frisch
                                                                                                                                                                                                                                                                                                                            Lycopersicon esculentum Eukaryota; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                      Alcala, C., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ames, IA 50011-1010 Phone: 515-294-6233 FAX: 515-294-2299
email: rcsshoe@iastate.edu"
a 79 c 114 g 134 t
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Search completed: June 23, 2000, 19:06:03 Job time: 27396 sec
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Best Local Similarity 66.3%;
Matches 299; Conservative
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                                                                                       ttacattgacacagaagttgagcagcttattcaagtagcattactctgtacccagggttc 1562
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/tissue_type="callus"
/tissue_type="callus"
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/lab_host="XL1-Blue MRF'"
/lab_host="XL1-Blue MRF'"
/note="vector: pBlueScript SK(-); Site_1: EcoRi; Site_2:
/note="vector: Glovannoni laboratory; cLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Aired callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"
59 a 91 c 135 g 139 t
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/clone="cleC3318"
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/cultivar-"TA496"
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1: gb_bal
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2: gb_bal
2: gb_pal
4: gb_pal
6: gb_pl
7: gb_pl
11: gb_pal
12: gb_pal
13: gb_tal
14: gb_ss
11: gb_pal
15: gb_v
16: gb_v
17: em_bal
18: em_v
19: em_bal
19: em_bal
19: em_bal
20: em_bal
21: em_bal
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-318.517 Million cell updates/sec
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45: gb_htg7:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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444	40 41 42	33 33 34 35 36 36 36	23 23 24 25 26 28	113 113 114 115 116 117 118 119 20	110987654321	No.
95.8 93.6	7 20	106.2 104.6 103.8 100.4 100.4 100.4 99.2 97.4	112 112 110.4 108 108 108 107.2 107.2	20004700000		Score
22.3	2222		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,			Query Match
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50	50 50	50 87 77 70 87 77	588857578	77888755	877855 77855	B
RICPRKI AC006569	AC007260 AB025636 AF058926 AC005312	ATHER AC004484 AC002334 AC006068 AB009053 AB019235 AP000559 AP000391 AC002392	AF024650 ATZ84202 AC006072 AB005240 E127052 ATU47029 ATAC009755 ATAC009755 ATAC011664 E12706	DC093048 DC093048 A67797 AB025639 AC005170 AB005234 F17123 SBRLK1 ATF8B4 ATF8B4 ATF10M6 AB018120	A67815 AC012654 AC012654 F23M19 F23M19 ATF17M5 A67796 AC002292 AB012245 AB012245 AB013395	ID
L27821 Oryza sativ AC006569 Arabidops	AC007260 Arabidops AB025636 Arabidops AF058826 Arabidops AC005312 Arabidops	4 4 0 10 40 10 10 10 10 10 10 10 10 10 10 10 10 10	A 5 A 7 0 7 2 . O	A67797 Sequence 2 A67797 Sequence 2 AB025639 Arabidops AC005170 Arabidops AB005234 Arabidops AF160182 Arabidops Y14600 Sorghum bic AL034567 Arabidops AL034511 Arabidops AB018120 Arabidops	115 1265 1745 196 196 198 198 198 198 198 198 198 198 198 198	Description

ALIGNMENTS

Qy 301 acaaaactcaaatctttcaatctctgccaaagttgggtttagaaagaa	181 tggtattgtgatgaaacagtagtaaagtcatactgggcacgccatactacttccacagtg		ery Ma st Loc tches	exon 12801367 exon 17961367 exon 17961328 exon 20142085 exon 20142085 exon 24502521 exon 24502521 exon 26172688 exon 26172688 exon 30153146 exon 30153146 exon 3053646 exon 37604081 BASE COUNT 1120 a 770 c 785 g 1406 t	õ	SOURCE thale cress. ORGANISM Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. REFERENCE 1 (bases 1 to 4081) AUTHORS De,V.S., Schmidt,E.D., Van,H.G. and Hecht,V.F.	RESULT 1 A67815 A67815 A67815 DOEFINITION Sequence 20 from Patent W09743427. ACCESSION A67815 VERSION A67815.1 GI:4756638 KEYWORDS .
1381 CAATTACTCAGCTTTACTCGTTTCTCAATTACTTTCTTTTTTTT	cattgttgtttgaaatggagtcgagttatgtggtgtttatcttactttcactg	GGATTTTATTTTTACTCTTTGTTTGTTTTAATCCTAATGGGTTTTTAA GCATTTTTATTTTTACTCTTTGTTTGTTTTTAATGCTAATGGGTTTTTA LLALGGAAAAALGAGLGAGLGALLLLLLLLLL	1021 gtgtgtgagagagagagtgtggtttgattgaggaaagacgacgagaaagacgcgggagaacgccgggagaacgccgggagaacgacg	GAGATCTTTAAAAATATTAATATAATATATCAACGAAAAAAGCTATTTATT	Qy 721 tacgggcagcttatattcctcgtcttcctcctctacaccactgcatgcccataaataa	601 tgcatagccttaagagctttcaactactttaccccaaagcgatgtcactttcaa	Qy 481 taactttactttcataaatacgggattacgaatcttacttgcattaaaaatttagaaaag 540

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1500	aatcgctatctttagtgtctgcattttgatttatgaaaattgttgttgttgttctttgtattt	1441	Qy
1440	CAATTACTCAGCTTTACTCGATTTCTCAATTACTTTCTCGATTCTTTTTTTT	1381	₽
1440		1381	Qγ
1380	CTTACTTCCGAATCATTCACTGTGGCTTGCTTCTGCTAATTTGGAAGGTTCGTGGTTACT	1321	B
1380		1321	Qy
1320	TTTAGCATTGTTTGAAAIGGAGTCGAGTTAIGTGGTGTTTAICTTACTTTCACTGAT	1261	뭥
1320		1261	Qy
1260	TGGTGATTTTCGGAAGTTAGGGTTTTCTCGGATCTGAAGAGTCAAATCAAGATTCGAAA	1201	ğ
1260		1201	Qy
1200	AAGGGTTATCGAAAAAATGAGTGAGTTTGTGTTGAGGTTGTCTCTGTAAAAGTGTTTAATGG	1141	₽
1200	aagggttatcgaaaaaatgagtgagtttgtgttgaggttgtctctgtaaagtgttaatgg	1141	Qy
1140	AATTAGGATTTTTAATTTTTTACTCTTTGTTTTTAATGCTAATGGGTTTTTAA		Дb
1140	aattaggatttttattttttttttactcttttgttttgt		Qy
1080	GTGTGTGAGAGAGAGAGAGTGTGGTTTGATTGAGGAAAGACGACGACGAGAACGCCGGAG		밁
1080		1021	Qy
1020	GCTCTTATTTTTTGTTTAAAAAAAAGTTTCATCTTTATTCAACTTTTTGTTTTACAGT	961	В
1020		961	Qy
960	GTTGCGGCTTAATAAAAAGCTCTTTTGTTATTATTACTTCACGTAGATTTTCCCCCAAAAA	901	及
960		106	VQ.
900	AGAAGAAAAAGAGGAACAACAACAACAACAATAGTTTCTCTGGCAGGCTTGTT	841	Db
900		841	Qy
840	CCCGTTGAGATCTTTAAAATATTAAATATATATCAACGAAAAAGCTATTTTATTCATA	781	뭥
840		781	Qy
780	TACGGGCAGCTTATATTCCTCGTCTTCCTCCTCTACACCACTGCATGCCCCATAAATAA	721	망
780	acgggcagcttatattcctcgtcttcctcctctacaccactgcatgcccataaataa	721	Qy
720	CCATCTCTTCTCCCCCGAACCCGTTTTTTTGACCGGTCAGTTCGGGCAGCAGCACCGT	661	В
720		661	δ.
660	TGCATAGCCTTAAGAGCTTTCAACTATTACCCCCAAACCCAAAGCGATGTCACTTTCAA	601	В
660		601	δÃ
600	GTTTTTCTACTTAAAGAAAAAAGGGACCCAACAGAGAGAG	541	В
600		541	Qγ
540	TAACTTTACTTTCATAAATACGGGATTACGAATCTTACTTGCATTAAAAATTTAGAAAAG	481	ф
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61 acaacagtctcactgggtcaattcctatgtcactgaccaatattactaccettcaagtgt 2520	atttctgtgagtatacatatgctttaccggctcagttacagtctttgtttaatcttaggt 240	cataactggcccgattcctagtaatcttggaaatctgacaaacttagtgagtttggatct 228 [01 gcatcatgctttaacaaaacaaatccaagatttgacagaagaagcactggagttaccttt 2160	81 taccgacatttttgtttcttttgtcaaatacagtgattttggggaatgcagagttatctgg 2040	61 cctacgctagtgaatccttgcacatggttccattgcaacaacgagaacagtgtc 1920	41 attagacttttcaccaattgatgctaattgtgtagatttgttgttcttgttataggtgat 1800	ttgatgttgttgatccaaacattctctgaaag 	162
	0	ОУ ОУ ОБ	2y 2y 6d	Db Qy Db	2 V V V V V V V V V V V V V V V V V V V	Qy Qy Qy	Qy Qy Qy	
y 3-41 gttcatcataacctgttcagattacgaggtttctgttargaccaccgaccgaggattgctt 3600 1 1 1 1 1 1 1 1 1	3421 aaagtctacaagggacgcttggcagacggaaotcttgttgctgtcaagagactgaaggaa 3	y 3301 gcagccgaagaagatccagaagttcatctgggacagctcaagaggttttctttgcgggag 3360	y 3181 gccagcaatttgttttgcagaaaagtattggaaaactgttaatggaaatcaata 3240	3061 tgctgctttgc 3061 TGCTGCTTTGC 3121 actagatattt 3121 ACTAGATATTT	ωωνκ	2821 CCTGGATCTCCCCGGTTTTCCCTCCACCACCTTTTATTCAACCTCCCCCAGTTTCCCACC 2	2701 atcctcttcagttatttcagttgttgtgtcagtgtctgaacttattctgaaactttcatt 2	0 2641 TGGTTCAGTTCCTGACAATGGCTCCTTCTCACTCTTCACACCCATCAGGTTCTATGATTT 2700

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Submitted (10-DEC-1999) Plant
Street, Albany, CA 94710, USA
On Dec 10, 1999 this sequence
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Liu,S.X., Lee,J.M., Sakano,H., Yu,G., Jhaveri,A., Lenz,C.,
Liu,S.X., Lee,J.M., Sakano,H., Yu,G., Jhaveri,A., Lenz,C.,
Toriumi,M., Chin,C., Chiou,J., Choi,E., Gonzalez,A., Howng,B.,
Koo,T., Li,J., Liu,A., Pham,P., Vaysberg,M., Altafi,H., Brooks,
Buehler,E., Chao,Q., Conn,L., Conway,A.B., Hansen,N.,
Johnson-Hopson,C., Khan,S., Kim,C., Lam,B., Nguyen,M., Palm,C.,
Shinn,P., Tambunga,G., Davis,R.W., Ecker,J.R., Federspiel,N.A.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="1"
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tgtgtgtgtgagagagagtgtggtttgattgaggaaagacgacgacgagaacgccgga 1079
                     AGCTCTTATTTTTTTTTAAAAAAAAAAAGTTTCATCTTTATTCAACTTTTTGTTTTTACAG
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79795	CCAGCAATTTTGTTTTGCAGAAAAGTATTGGAACAACTGTTAATGAAAATCAAI	_
3239	Qy 3180 agccagcaattttgttttgcagaaaagtattggaacaactgttaatgaaaatcaatacat	
79735	QY 3120 cactagatattticttcgatgqtgcctggtgagtttattattcgcattagtttctgttctt	
96	79616 GTGCTGCTTTGCTGCTGCTGCTGCAATAGCCTTTGCTTGGTGGGGACGAAGAAAG	
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39	2880 cccgagtaagcctcctctttttagtttacattataggaaacagaagatgaaatctttgc	
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2879	Qy 2820 teetggateteeceegtttteteeteeaceattttatteaaceteeceeagttteeac	
79375	79316 TTCCTTGTGCAGTTTTGCTAATAACTTAGACCTATGTGGACCTGTTACAAGTCACCCAT	
2819	teettytyeayttttyetaataaettayaeetatytyyaeetyttaeaa	
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	ngtetcactgggtcaattcctatgtcactgaccaatattactacccttcaac	
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79015	TTTGTTCCAATTTTTGACTCTTTGCTGAAAATTTTTACATGCAAGAATAGCCGGCTTAA	
2459	ttccaatttttgactctttgctgaaaattttacatgcaagaatagccggctt	
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78895	Db 78836 TTTACTTAAACAGCTTCTCCGGTCCTATTCCGGAATCATTGGGAAAGCTTTCAAAGCTGA	
2339	ttacttaaacagcttctccggtcctattccggaatcattgggaaagctttcaaagctg	
78835	Db 78776 ACATAACTGGCCCGATTCCTAGTAATCTTGGAAATCTGACAAACTTAGTGAGTTTGGATC	
2279	2220 acataactggcccgattcctagtaatcttggaaatctgacaaacttagtgagtttggat	
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Sequence :
A67827
A67827.1
Arabidopsis thaliana 
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; 
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
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De, V. S., Schmidt, E. D., Van, H.G. a
PRODUCTION OF APOMICTIC SEED
Patent: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
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PKMSEVVRMLEGDGLAEKWDEMQKVEILREBIDLSPNPNSDWILDSTYNLHAVELSGP
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1 (bases 1 to 88401)
Vysotskaia, V.S., Schwartz, J.R., Yu, G., Toriumi, M., Lenz, C., Liu, S., Lee, J., Liu, A., Li, J., Kremenetskaia, I., Luros, J., Gonzalez, A., Altafi, H., Araujo, R., Chao, Q., Conn, L., Conway, A.B., Dunn, P., Hansen, N., Hulzar, L., Kim, C., Palm, C., Rowley, D., Shinn, P., Walker, M., Davis, R.W., Ecker, J.R., Federspiel, N.A. and Theologis, A. Arabidopsis thaliana chromosome 1 BAC F23M19 sequence Unpublished (1999)
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AC007454
AC007454.3
                                                                                                                                                                                                                                                                                                  Submitted (17-JUN-1999) Plant Gene Expression Center, 800 St., Albany, CA 94710, USA On Jun 17, 1999 this sequence version replaced gi:4996902. The sequence of BAC F33M19 from Arabidopsis thaliana chrom
                                                                                                                                                                                                                                                                                                                                                                                                            submitted (04-JUN-1999) Plant
Street, Albany, CA 94710, USA
4 (bases 1 to 88401)
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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3 (bases 1 to 88401)
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Direct Submission
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/gene="F23M19.1"
complement(j0in(796. .1116,1205. .1271,1349. .1432,
1506. .1636,1794. .1850,1999. .2047,2166. .2251,2468.
2771. .2893,2990. .3079,3154. .3254,3332. .3393,3467.
3638. .3891))
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                                  PF|00561 alpha/beta hydrolase fold
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene
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                                                                                                                                                                                                                                                                                                                                                                                               complement(43028. .48860)
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genome
gi|836774 FAB1 protein
me gb|D50617."
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                                                                                                                                                                                                                                                     Submitted (11-MAR-1999) MIPS, at the Max-Planck-Institut fuer Blochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schuelle@mips.biochem.mpg.de,mapg.de.mapg.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosome 4 can by viewed at: http://websvr.mips.biochem.mpg.de/proj/thal/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphylophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.

1 (bases 1 to 96475)

Bevan, M., Rose, M., Hempel, S., Entian, K.-D., Hoheisel, J.,
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/variety-"Columbia"
/db_xref-"taxon:3702"
/chromosome-"4"
2377. .3928
complement(join(2377...2571,2755...2837,3032...3098,
3180...3230,3461...3574,3668...3724,3815...3928))
/note-"similarity to Caenorhabditis elegans cosmid, gene
T16G1.11, pID:e1349366; contains EST gb:T20620, N65143,
T45799, H36819, R65238, N37318"
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/note="strong similarity to WD-repeat protein carota, PID:92253631; Contains Trp-Asp (WD-40) signature [VLAIALDHTVYLWDA] [TGGGGGDRTIKFWNT] [VASAAGDETLRFWNV]"
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slevnlcllrlyqfepermnihivarilvkalmampipdfslclflipervqmeeqfk
slivlshyleigrfqqfwdeaaknrhileavpgfeqaiqayashllslsyqkvprsvl
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/number=6
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                                                                                                                                                                                                                                                                                                                                             /translation="MDAGLNRCPLQEHFLPRKNSKENLDRFIPNRSAMNEDYAHFALT EERKCKDQSAMVSSPSKEAYRKOLAFFMNLNHFRILAFENRFOAFVELLPSNHSASIH QOPKSVKPRYIPQTSERTLDAFDIVDDFYLNLLDWGSANVLAIALDHTVLMDSRYG STSELVTIDESKGFUTSINMAPDGRHYAVGLNNSEVOLWDSASNROLRFLKGGHOSRV GSLAWNNHILTTGGMDGLINNDVRIRSPIVETYRGHTQEVCGLKWSGSGQQLASGGN DNVVHIWDRSVASSNSTTQWLHRLEEHTSAVKALAWCPFQANLLATGGGGGDRTIKFW
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5815. .6093,6423. .64
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/gene="F17M5
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                                                 complement(6423.
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                /gene="F17M5.50"
12884. 14176
/gene="F17M5.50"
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RKRHFNPDDVFTTPNQQLVISPPVDNELEDLIDIDLDFDIDKILNFLLVASHTGYEQE
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9139...9417,9803...99
                                                                                                                                         complement(12458.
                                                                                                                                                                         complement(11587.
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LSLAKRAISPDGFLVFMKRSHVVSKCFLTIPYKMCVKNMLITRQEVVMQVDQTKWEMK
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/gene="F17M5.40"
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'note-"strong similarity to Arabidopsis thaliana
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tttttaagttacaaactcttttgagtaaaatctcgattgcaaaatctctatgcagccga 3308
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                                                                                                                                                                                                                                                                                                                             CATTGCGACCCAAAGATTATTCATCGAGATGTGAAAGCTGCAAATATTTTGTTGGATGAA 50615
                                                                                                                                                                                                                                                                                                                                                             TGGCCAAAGAGACAGCGTATTGCGTTGGGATCTGCAAGAGGGCTTGCGTATTTACATGAT
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REENSDGYNHIICFDFTRERFGPLLPLPVNVIDNEYEYVTSSCVREGKIAALFQHNDS
YPYELEIWITTKIEAEMYSWNRFLRIDIEPNNNIMVPFIYGGFFIDEEKKKVALGFDE
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HIGKVTSTREGESRVIMLIDYNLFLMSAVLMDDVDPSIEFKGKLSCLKEQVKISQVFH
CEGLLLCILKDDTRIVVMNPYRQETKWIIPRYSHRPYVMNNIRYALGYENNKSGRSLK
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/codon_start=1
/product="hypothetical protein"
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/db_xref="GI:4490296"
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Pred. No. 5.3e-65;
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Best Local Similarity 57.8%;
Matches 903; Conservative
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           taacttagacctatgtggacctgttacaagtcacccatgtcctggatctcccccgttttc 2840
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                                                 GAAAGCTATGATAATATTTTTTTTCTCCTTCATATATTATCACTTTCGCAGTTTTGGCAA
                                                                     tgaacttattctgaaactttcatttc----
                                                                                                  TACACCTATCAGGTTTAATGCTAGTAATATCTTTAATATTATGGTTCTTACTTCTACTGC
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.

1 (bases 1 to 6695)

De,V.S., Schmidt, E.D., Van,H.G. and Hecht,V.F.

PRODUCTION OF AFOMICTIC SEED Patent: WO 9743427-A 20-NOV-1997;

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Sequence 1 from Patent W09743427.
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A67796.1 GI:4756622
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1182 c 1243 g 2421
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Pred. No. 1.3e-63;
0; Mismatches 506;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscar-SE (Sean Eddy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medical Center Dr., Rockville, MD 20850, USA
On Dec 17, 1999 this sequence version replaced gi:4726109.
The sequence and annotation of the sequence and annotation of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jining Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xqrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes were identified by a combination of three methods: Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                    This work was supported by the National Science Foundation, 
Department of Energy and the US Department of Agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are numbered from the top to the bottom of the chromosome.
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                                                                                                                                                                                                                                                                                 all correspondence to:
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/cultivar-"Columbia"
/note="Sequence from clone F13J11"
                                                                      /db_xref="taxon:3702"
/chromosome="2"
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/gene="At2g13690"
/note="F13J11.4; predicted by genscan and genefinder"
complement()oin(14929. .15843,16401. .17114))
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NVIKKFMTMGVYRAIDVLEVAAGIKTSRAVLSCLKYLEAVPWTEDEEEKKRLLGIS
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VYEKEQPEINKEDIYARGKCCVDSLAKLFEEGSSSSSSKKEKDLIESISREVENINML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAD28311.1"
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KSEKVERVAPEJIAAARDVOEKERIYAPYNLFLDSRAAGASGYMQLEEVKAAVAALG
KSEKVERVAPEJIAAARDVOEKERIYAPYNLFLDSRAAGADDIQQRKILYMGLYLLI
TRGLNWPSGFEQHRKKTGNLDLLDWLRAMFGFQASWLPQAAQDIQQRKILYMGLYLLI
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SPPRNLYLCLRLYLLAFCHRSPEEIEQDEDSNSSYSVPINRINLINPPRRTDALNKPF
WRSKELPSLGRRIKHSMNKDPFDDFWNFHLPEIGRVNLSLQKATKRERKKVNPNKSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(<14929. .15843,16401.
/gene="At2g13690"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10367. .13711
/gene="At2g13680"
/note="F13J11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(517. .842,907. .1114))
/gene="At2g13660"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(451. .842,907. .1234))
/gene="At2g13660"
                                                                                                /rpt_family="POLY_A" complement(29932. .3 /gene="At2g13710"
                                                                                                                                                                                                                                                                          complement(18082.
/gene="At2g13700"
/note="F13J11.5"
                                                                                                                                                                                                                                                                                                                                                                                        WFSKHGTECPNLSKAFQIWWRRSFLRGVESSTCR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIYRVVQTVQV"
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join(3349. .3541,3644. .3744,4109. .4230,4375. .4471,
4583. .4693,4792. .4928,5629. .5755,5848. .5997)
/gene="At2g13670"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEIMIDREIAEEFVEIWGKQRRLVEMHERVSPMVRYEVSRVTGAIFIAMGKRRVQCGG
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                                                                         note="F13J11.6"
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                                                                                                                                                                                              | 999aaagtctacaagggacgcttggcagacggaactcttgttgctgtcaagagactgaag
                                                                                                                                                                                                                                                       GAACTGCTAGTTGCTACAGAGAAATTTAGCAAAAGAAATGTATTGGGCAAAGGACGTTTT
                                                                                                                                                                                                                                                                             gagctacaagtggcgagtgatgggtttagtaacaagaacattttgggcagaggtgggttt 3417
                          gaagagcgaactccaggtggagagctccagtttcaaacagaagtagagatgataagtatg
                                                                                                                                                                      GGTATATTGTATAAAGGACGTTTAGCTGATGACACTCTAGTGGCTGTGAAACGGCTAAAT
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complement(<33782...>34228)
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complement(33782...34228)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAD28314.1"
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AABPRRTLGDFNRPGMEYANRSAIVPPPYQRNDYESHLFYYITLHI"
complement(35689. .35776)
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36924. .37497
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QVMREKNVLSNVDQNKRFFIWDEGSEAALENAFGTSEDKQKKWIEKYVPGTFLDSKKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="At2g13720"
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="At2g13720"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="At2g13740"
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.>33473
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 375.6; DB 50;
Pred. No. 1.5e-61;
0; Mismatches 244;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
euphyllophytes; Spermatophyta; Magnollophyta; Embryophyta;
euphyllophyta; Prassicales; Brassicaceae;
                                                                                                                                                                                                    i (bases 1 to 120787)

I (bases 1) to 120787)

Rederspiel, N.A., Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R., Au, M., Araujo, R., Brendel, V., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Oji, O., Osborne, B.I., Shinn, P., Sun, H., Toriumi, M., Ysotskaia, V.S., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Genomic sequence of Arabidopsis

Unpublished (1997)

2 (bases 1 to 120787)

Federspiel, N.A., Davis, R.W., Conway, A.B., Palm, C.J., Conway, A.R., Kurtz, D.B., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Shinn, P., Sun, H., Oji, O., Osborne, B., Shen, Y.K., Toriumi, M., Vyotskaia, V., Pirof, Shinsissin, P., Palm, C.J., Theologis, A. and Ecker, J.
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AC002292
Federspiel, N.A., Davis, R.W., Conway, A.B., Palm, C.J., Kurtz, D.B., Buehler, E., Dewar, K., Feng, J., Kim, C., E. Sun, H., Oji, O., Osborne, B., Shen, Y.K., Toriumi, M., V. Yu, G., Theologis, A. and Ecker, J. Direct Submission
                                                                                                                                                Submitted (05-JUN-1997) Biochemistry, Sequencing and Technology Center, 855
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                                                                                                                                                Stanford University/DNA California Avenue, Palo
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., Conway, A.R., Li,Y., Shinn, P., Vyotskaia, V.,

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6 (bases 1 to 120787)
6 (bases 1 to 120787)
Federspiel, N.A., Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Au, M., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Oji, O., Osborne, B.I., Shinn, P., Sun, H., Toriumi, M., Vyotskaia, V., U, G., Ecker, J., Theologis, A. and Davis, R.W.
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Submitted (09-UUL-1997) Biochemistry, Stanford University/DNA
Sequencing and Technology Center, 855 California Avenue, Palo Alto,
CA 94304, USA
5 (bases 1 to 120787)
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4 (bases 1 t
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                                                                                                                                                                                                                                                   /protein_id="AAB71970.1"
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GLRKVXSAYPLVVAMLPDVPEBHREILKSQGCVVREIEPVYPDNGVEFAMAYYYLNY
SKLRIMNFEEYSKMIYLDADIQVFDNIDHLFDLSDAYFYAVMDCFCEKTWSHSLQYSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HWYHNQYPTRQKNGPGISLLKKGIKNALDNLKAKHEGFLLSSHSRKICSYVPDLARSI
AGLIFSSTDLDFQGDCLSVLGFQTQEVERDTVENYIQRKIVTVIGMNERKPQKDQEAA
PFLFFDGESETSFFEDEEVEDRENSTHEYDATATKAYTQFKCLATMLQE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAB71954.1"
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complement(join(8347. .8443,8539. .8657,8941. .9066))
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                                                                                                                                                                                         GYCQQCPEKVTWPEDMESPPPPLYFNAGMFVFEPSPLTYESLLQTLEITPPSPFÄEQD
FLNMFFEKYYKPIPLYYNLVLAMLWRHPENVELEKVKVVHYCAAGSKPWRYTGEEANM
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complement(join(3171. .3389,3471.
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1845. .259,2256. .2526,2788. .2876)
/gene=""7815.1"
/note="Hypothetical protein"
                                                                                            complement (8347. . 9066)
                                                                                                                                                                 DREDIKMLVDKWWDVYNDESLDFKSKIPADAEETVTKSSILASVLEPEMTYFPAPSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="nearly identical to
protein gp|D26537|537404"
                                                             /gene="F8A5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="F8A5.1"
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/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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complement(join(9782. 9919,10031. 10178,10275. 10509. 10663,10780. 10917,10991. 11164,11286. 11815. 111936,12047. 12182,12300. 12395,12475. 12803. 12981,13104. 13313,13414. 13572,13659. 13867. 13983,14069. 14180))
/gene="F8655.4"
/note="location of EST gb|W43464"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAĞVPDLİMYDLIĞİTRYPVNĞQPENİYEQİSĞMİMEYLEDÇESİLLNYLSATVDFTT
CESIRKSKYUKTĞQRTLAVYTKADMAPEĞLLQKVTADDVSİTLĞYVCYRNRIĞEETY
EEARMQEELLFRTHPVLSLIDEDLİYGİPVLAĞKLMLIQSAMİARCLPKİVSKINĞKL
EAVLELNKLPMYMASTGEALMALMDIĞSAKESLLRILVĞĞDE'SEYPDĞUMKCTARL
ADMLSQFSDSLQAKPKEVAEFLMDEİKİLDECKCUĞLPNFİPRSAFLAILSQHYDĞĞİQ
DKPUEFINKİMDYİEDYLSSYTAKRSDNFPQIQSSİKBAĞRNLIŞKİKBQSVNRYMEİ
                         /translation="MGGSKKHVVTRTSSPSLAIVQANPHDNREVVPIEAPIISSYNDR
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PLVMRLQRSSSPVPEMLEYSDKIVPTDEEHIALAICAATDVIAGWGPISYHGRSSFY
NSRPVNGQPENIYEQISGMIMKYIEPQESIILNVLSATKPHWRRAYEQARMQEELLFR
THPMLSLIDEDIVGIFVIAGKUMLIQATMISRCLPEIVRKINKETAVLELNKLPMV
MASTGEALMALDDIIGSAKESLFRILVQGDFSEEFDDOWHGTARLADMISGSEDLLG
EKPKEVTEFLMNEIKILDECKCVGLPNFIPRSAFLANILSQHEDDAIHVKPVEFIKKIWD
                                                                                                                                                                                                                                                                                                                                                          //gene="F8A5.6"
join(18712. 19150,19685. .19839,19981. .20987,21054. .21188,
21973. .22091,22335. .22510)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDGGGVEKMLEESPLVASKREKLQNSIKLLKESKDAVAAIVDQNC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEMEKLTDYTCNPEYMTSWTQKTSAQESFIDAVVKNENIPDYFSVTGFGNVKISHLRK
YHAHLLIPAFDMKMRITSYWKIVLRRIVDNLALYLQLSVKSLVNTRFQKEIVAEMVDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VMRLQRSSSPEPEIWLEYNDKVVPTDEEHIAEAIRAATDVIAGSGKGVSDAPLTLHVK
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/codon_start=1
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join(15572. .1
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ekkpelyiecalyidgapfglpmrtrlkttgppycwnelitlsskyrdltahsqlait
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="Phosphatidylinositol 3-kinase"
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/db_xref="GI:2462752"
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LRDAVLLVFANKQDLPNAMNAAEITDKLGLHSLRQRHWYIQITCATTGEGLYEGLDWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative ADP-ribolylation factor
/protein_id="AAB71955.1"
/db_xref="GI:2462736"
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Y I EVVLSSVIAKY SENF PQ I QSA I KRAGRNL I TK I KEHSVERVLE I VEMEKLT DY TCN
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/db_xref="GI:2462737"
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                                                                                                                                                                                                                                                                                                                             /note="similar to "Mx" GTP-binding proteins"
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CDS gene

SGS

gene

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                         ataaagacactcacgtgacaacagcagtccgtggcaccatcggtcacatcgctccagaat 4017
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ATAGAGACTCTCATGTCACAACTGCAGTCCGTGGAACTGTTGGCCCACATTGCACCTGAGT
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/db_xref="G1:2462738"
/db_xref="G1:2462738"
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/t-aanslat.ton="McGSKMSNDYEIDVEAGMSSLSIVNTPIEAPIVSSYNDRIRPLL
DTVDRLRNLNYMREGIOLPTIVVVGDQSSGKSSVLESLAGINLPRGQGICTRVPLYMR
LQRSSSPEPEIWLEYSDKVVPTDEEHYAABICAATDVLAGTGSCVSDTPLTLSVKKNI
LQRSSSPEPEIWLEYSDKVVPTDEEHYABAICAATDVLAGTGSCVSDTPLTLSVKKNI
VPDLTMYDLPGJTRVPVMGQPENIYBQJESRMLMKYIEPQESIILNVLSAFUDFTTCES
IRMSRQVDKTGERTLAVVTKADMAPEGLLQKVTADDVSIGLGVICVRNRIGEETYEEA
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join(33787. .24210,24676. .25157)
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/gene="F8A5.8"
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                cgagtgatgggtttagtaacaagaacattttgggcagaggtgggtttgggaaagtctaca 3430
                                                                           caggtggagagctccagtttcaaacagaagtagatgataagtatggcagttcatcgaa 3550
                                                                                                                                     CAACAAGCAATTTTAGTCCAAAGAACATTTTGGGACAAGGAGGGTTTGGGATGGTTTATA 72060
                                                                                                                                                                                                                                          AAGACTACGAATTTGAAATCGGCCATCTGAAAAGGTTCAGTTTTCGCGAAATACAAACCG 72120
ACCTTTTACGCCTCTTTGGATTCTGTATGACCCCGGAAGAGAGAATGCTTGTGTATCCGT
                                                         ATACAGGAGAAGTTCAGTTTCAAACCGAAGTAGAGATGATTGGCTTAGCTGTTCACCGTA
                                                                                                                     AAGGGTATCTCCCAAATGGAACTGTGGTGGCAGTTAAAAAGATTGA---AAGATCCGATTT 72003
                                                                                                                                                                                                                                                                                                       484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-MAR-1998) to the DDBJ/EMBL/GenBank databases. Yasukazu Nakamura, Kazusa DNA Research Institute, Laborator Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935, Fax:+81-438-52-3934)
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/strain="Columbia"
/db_xref="taxon:3702"
/chromosome="5"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyliophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                   Submitted (06-MAY-1998) to the DDBJ/EMBL/GenBank databases. Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory Gene Structure 2, 1532-3, Yana, Kisarazu, Chiba 292, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935,
                                                                                                                                                                                                                                                               Direct Submission
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Unpublished (1998)
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Arabidopsis thaliana (strain:Columbia) DNA,
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/strain="Columbia"
/db_xref="taxon:3702"
/chromosome="5"
/clone="MXNN23"
/clone=11b="Mitsui p1"
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ACCESSION VERSION KEYWORDS

ORGANISM

carrot.

Daucus carota

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.

RESULT 1

DEFINITION

DCU93048

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mRNA embryogenesis

receptor-like

28-JUN-1997 kinase mRNA

Daucus carota somatic complete cds. U93048 U93048.1 GI:2224910

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                                              aatggactataaagacactcacgtgacaacagcagtccgtggcaccatcggtcacatcgc
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                                                                                                    GGTAGATGTTAGAAGGACTAATGTAACCACTCAGGTCCGAGGAACAATGGGTCATATTGC
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                                                                          ttatgggttcataattgttggttacactaatgacacagagagggccaccgtcacaacctcc
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Development 124 (10), 2049-2062 (1997)
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Schmidt, E.D.L., Guzzi
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VRGTLGYIAPEYLSTGKSSEKTDVFGYGJMLLELITGQRAFDLARLANDDDVMLLDWV
KSLLKEKKLEMLVDDPLENNYLDTSEVEQLIQVALLCTQGSPMERPKMSEVVRMLEGDG
LAEKWDEWQKVEVIHODVELAPHRTSEWILDSTDNLHAFELSGPR*

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  504;
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Sequence 2 from Patent W09743427.
A67797
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  Conservative
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94. .1755
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354 c 415 g 515 t
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Score 270.8; DB 5;
Pred. No. 1.5e-41;
0; Mismatches 157;
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Structural Analysis of
Unpublished (1999)
2 (bases 1 to 84896)
                                                                                                                                                                                                                                                                                                         complete sequence. AB025639 AB025639.1 GI:4589 HTG.
                                    Direct Submission
Submitted (02-APR-1999) to the DDBJ/EMBL/GenBank databases.
Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory
Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan
(E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935,
Fax:+81-438-52-3934)
                                                                                                                                                                                                                    Arabhdopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Arabidopsis thaliana
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 /organism="Arabidopsis
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/db_xref="taxon:3702"
/chromosome="3"
/clone="MMIL2"
/clone_lib="Mitsui P1"
a 15039 c 15617 g 26
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Pred. No. 2.4e-40;
0; Mismatches 253;
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26980
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AUTHORS
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ORGANISM
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                                                                                  FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit, 'ftp.genome.washington.edu/RW/RepeatMasker.html). Genes are numbered from the top to the bottom of the chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D., Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E., Feldblyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M., Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayam,L., Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H., Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D., Mierman,W.C., White,O., Elsen,J.A., Salzberg,S.L., Fraser,C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC005170 AE002093
AC005170.2 GI:65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (13-DEC-1999) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA On Dec 17, 1999 this sequence rersion replaced g1:3738313. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lin,X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 402 (6763), 761-768 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                               like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                                                                                                                           F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would
                                                                                                                                                                  This work was supported by the National Science Foundation. 
Department of Energy and the US Department of Agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 We thank the CSHL/WashU/ABI consortium for sequencing BAC clones
                                                                                                                                                                                                                                                 database support.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 110211)
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                                                                                                          all correspondence to:
  /organism-"Arabidopsis thaliana"
/cultivar-"Columbia"
                                                                               Location/Qualifiers
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                                                          .110211
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complement(4565...4612)
/rpt_family="(CAA)n"
6379..6484
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/note="Sequence from clone F27L4"
complement(356. .401)
/rpt_family="(TAA)n"
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8152. .8268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MFLLILLVFCITVFAFVVTNKGAGEAIEGKGYKEXKLGDYSTWL
GKRVENGKNNNKIRSCLVESKYCSKLEAKFYNVPVNSFYKEHLTALQSGCCKPSDECG
FEYYNPTTWRKNTTGTHTNDPOQTWNDAKEKLCFDCQSCKAGLLDNVKGAWKKVAIVN
IVFLVFLIIVYSVGCCAFRNNKRDDSYSRTYGYKP"
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/gene="At2g23810"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(1549. .2058,2731. .3012))
/gene="At2g23810"
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/note="F27"
                                                                                                                                 /translation="MSNNELLEIEPMYLQFFEELKKQMSCSLYLTNKTDNNVAFKVKT TNRNNYCVRPMYGLILDKSTCKVLVTMQAQKEVPSDMGSFEKFMIQSVLASPGVTAKE VTREMFSKESGHVVEETKLRVTYVCSTTTNITSSPRTRRGFIFQCFC" complement(11332 ...11371)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <6480. .8786
/gene="At2g23820"
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/protein_id="AAF18611.1"
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/chromosome="2"
                             /rpt_family="
15853. .15918
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KNRRESEALEHMCKLLGGGERAKETAELMREYEENSSPEAKVVKDFDKVELTLQALEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mknvnrvffckslslvflvpsftrshirftysaagasspnraih
CMASDSPQSGDGSVSSPPnvaavpssssssssassaidflslctrlkttpragwikrdv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(6480.
8152. .826
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join(<6480. .6749,7602.
8152. .8268,8487. .8786)
/gene="At2g23820"</pre>
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/note="Sequence from_clone T29E15"
                                                                                     /rpt_family-
15801. .1591
                                                                                                                                                                                                                                                                                                                                                                                                                         join(9531.
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<9531. .>10396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQGKFQTNIGKAWASEIVSRRRKQH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAC63656.1"
/db_xref="GI:3738315"
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8152. .8268,8487. .8557)
/gene="At2g23820"
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/db_xref="GI:3738316"
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/note="unknown protein"
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/rpt_family="(CAAAA)n'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene-"At2g23830"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="T29E15
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Best Local Similarity
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             gtaacaagaacattttgggcagaggttgggtttgggaaagtctacaagggacgcttggcag 3445
                                                 GTTGGGAAATCTAAGAAGCTTCACATTCAGGGAACTTCATGTAGCTACGGATGGTTTTA
                                                                          atctgggacagctcaagaggttttctttgcgggagctacaagtggcgagtgatgggttta 3385
                                                                                                                                  tttgagtaaaatctcgattgcaaaatctctatgcagccgaagaagatccag---aagttc 3325
                                                                                                                                                              TTCGCATTAGTGGTTAGTCAAATCGAGTAAGCTTATGGTTTATGTAATTTGATTTTGTTT 54373
                                                                                                       GTTCCAAGAGTATTCTTGGTGCTGGTGGGTTTGGTAATGTCTACAGAGGAAAATTCGGGG
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/rpt_family="(TAAAA)n"
complement(join(<20442.
                                                                                                                                                                                                                                                                       complement(join(<31877..32176,32267..32407,32498..32893,
33162..35713,35886..>36147))
/gene="At2g23880"
/gene="At2g23880"
/note="T29E15.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(22086. .22781)
/gene="At2g23850"
/note="T29E15.5"
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/db_xref="G1:3738317"
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CFRGLVLDISYRPVNVCWKRAICLEYMDKADVLEYYDQTVSSPTGSFYIPAVLRVPH
LLQVVKRRRVKNSLSKKNILLRDDYTCQ"
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31472. .
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vkaspavtakevtletenkesghlveetklrviyvcsttinitspprtrnglifnvfv
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/codon_start=1
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/gene="At2g23860"
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/note="T29E15.6"
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Pred. No. 2.5e-38;
D; Mismatches 316;
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                                                                                                             Sato, S., Kotani, H., Nakamura, Y., Kaneko, T., Asamizu, E., Fukamiyajima, N. and Tabata, S.
Structural analysis of Arabidopsis thaliana chromosome 5. I.
Sequence features of the 1.6 Mb regions covered by twenty
physically assigned Pl clones
physically assigned Pl clones
DNA Res. 4 (3), 215-230 (1997)
                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Submitted (02-JUL-1997)
                  Nakamura,Y.
Direct Submission
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                                            tctctcaaccggaaaatcttcagagaaaaccgacgttttcggatacggaatcatgcttct 4078
                                                                                     ATCTCTGACTCATGTCACAACTCAAGTCCGAGGCACAATGGGTCACATTGCGCCAGAGTA 55185
                                                                                                      taaagacactcacgtgacaacagcagtccgtggcaccatcggtcacatcgctccagaata
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                            TCTCTGCACAGGAAAATCATCTGAAAAAACCGATGTTTTTGGTTACGGTATAACGCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory of Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935, Fax:+81-438-52-3934)
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/strain="Columbia"
/db_xref="taxon:3702"
/chromosome="5"
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16340 c 16159 g 28865
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Search completed: June 24, 2000, 00:12:15 Job time: 45690 sec

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Sequence 4081 BP; 1120 A; 770 C; 785 G; 1406 T;
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Best Local Similarity 100.
Matches 4081; Conservative
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	2640		Db 25
	2580	521 tgtgagtcctctcattaactttcatttatgtctacttcattctccctcagttgatttgtt	Qy 25
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	2520	461 acaacagteteaetgygteaatteetatgteaettgaeeaatattaetaeeetteaagtgt	Qy 24
	2520		Db 24
	2460	401 tttgttccaattttttgactctttgctgaaaattttacatgcaagaatagccggcttaaca	Qy 24
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	2400	341 atttctgtgagtatacatatgctttaccggctcagttaccgtctttgtttaatcttaggt	Qy 23
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	2220	161 tgtaattgaaatctttttaacaagtttcttattttcttacagggagctttacagtaacaa	Qy 21
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	2040	981 taccgacatttttgtttcttttgtcaaatacagtgatttggggaatgcagagttatctgg 	ДУ 19 Дъ 19
	1980	921 ataagagtgtaaagctttcttctactaatcccactttttaaactttgacctcagcgtggt	Qy 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Production of apomictic seeds - useful in plant breeding Production of apomictic seeds - useful in plant breeding Claim 27; Pages 91-95; 123pp; English.

It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed apomictic plant selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated.

Apomixis allows plant breeders to develop cultivars with seed and forzage quality and maturity.

Sequence 2089 BP; 568 A; 419 C; 503 G; 599 T;
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 13.;
Best Local Similarity 85.;
Matches 664; Conservative
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V06591;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK gene.
receptor kinase; apomixis; apomictic; se
plant breeding; ds.
Arabidopsis thaliana.
Key
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20-NOV-1997.
13-MAY-1996; GB-010044.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De VY168 SC, Hecht VFG, $
WPI: 98-086529/08.
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plant parts; and (c) expressing the sequence in the vicinity
of the embryo sac. The apomictic seeds and embryos thus produced
can be developed into plant progeny. This is useful in plant
breeding programs. Controllable and reproducible apomixis provides
many advantages in plant improvement and cultivar development in
the case that sexual plants are available as crosses with the
propagated hybrids and could shorten and simplify the breeding
propagated hybrids and could shorten and simplify the breeding
process so that selfing and progeny testing to produce and/or
stabilise a desirable gene combination could be eliminated.
Apomixis allows plant breeders to develop cultivars with
specific stable traits for such characteristics as height,
seed and forage quality and maturity.

Sequence 6695 BP; 1844 A; 1182 C; 1243 G; 2422 T;
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Best Local Similarity
Matches 903; Conserv
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20-NOV-1997.
13-MAY-1997; E
14-MAY-1996; C
(NOVS) NOVART
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The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating
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De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;

WPI; 98-086529/08.
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tgaacttattctgaaactttcatttc--
                              TACACCTATCAGGTTTAATGCTAGTAATATCTTTAATATTATGGTTCTTACTTCTACTGC
                                                                                                                                                                      CTAATATTACAACTCTTCAAGTCCTGTAAGTATTCCGACCTTTCCAGATAGTT-----
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                                              cacacccatcaggttctatgatttatcctcttcagttatttcagttgttgttgtcagtgtc
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                                                                                                                                                 -TTGTTGTTGTGGATGTTTCAATTTTAATACTAAATATGTTCATCAG
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-----cttgtgcagttttgctaa
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3741 g 3741 5398 G 5398	dp dy
3681 totoaattactttgacgtgaagtgtttttttcatgtttttcctttatgggttcataattgtt 3740	dg Qy
3621 tggaagtgttgcttcgtgtctcagaggtaaaaactaaacaattaaacatcttgtgctctc 3680 	ου
3561 attacgaggittctgtatgacaccgaccgagagattgcttgtgtatccttacatggccaa 3620	Qγ
3501 gctccagtttcaaacagaagtagagatgataagtatggcagttcatcgaaacctgttgag 3560	Оy
3441 ggcagacggaactcttgttgctgtcaagagactgaagggaagagcgaactccaggtggaga 3500 	do V
3381 gtttagtaacaagaacattttgggcagaggtgggtttgggaaagtctacaagggacgctt 3440	ρδ
3321 agttcatctgggacagctcaagaggttttctttgcggggagctacaagtggcgagtgatgg 3380	Дb
3261 caaactettttgagtaaaatetegattgcaaaatetetatgcagecgaagaagatecaga 3320	Db Qy
3201 gaaaagtattggaacaactgttaatgaaaatcaatacataagtcattgttttttaagtta 3260	Db Db
gtttattattcgcattagtttctgttcttagccagc 	ρb
3081 ctcctgcaatagcctttgcttggtggcgacgaagaagccactagatattttcttcgatg 3140	Db Oy
3021 atggtataactggagcaatagctggtggagttgctgcaggtgctgctttgctctttgctg 3080	Db Qy
2961 atataaotcatottgocaataaggoaataaccaaatgatotaatttgatttoaggtgggt 3020	Db dy
2901 tagtitacaitataggaaacagaagatgaaatcitttgcitctctgtcaatccttittctc 2960	DB Qy
2841 tectecace&cettttatteaacetececcagtttecacecegagtaagcetectetttt 2900	Db dy
2781 taacttagacctatgtggacctgttacaagtcacccatgtcctggatctcccccgttttc 2840	0y .
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Production of apomictic seeds - useful in plant breeding
Production of apomictic seeds
CC CIAim 21; Pages 47-51; 123pp; English.
CC It may be used as part of a method of producing apomictic seeds
CC comprising: (a) transforming plant material with a nucleotide
CC comprising: (a) transforming plant material with a nucleotide
CC cell membrane renders the cell embryogenic; (b) regenerating
CC the transformed material into plants or carpel-containing
CC plant parts; and (c) expressing the sequence in the vicinity
CC of the embryo sac. The apomictic seeds and embryos thus produced
CC can be developed into plant progeny. This is useful in plant
CC treeding programs. Controllable and reproducible apomixis provides
CC many advantages in plant improvement and cultivar development in
CC the case that sexual plants are available as crosses with the
CC apomictic plant. Apomixis provides for true-breeding, seed
CC process so that selfing and progeny testing to produce and/or
CC stabilise a desirable gene combination could be eliminated.
CA pomixis allows plant breeders to develop cultivars with
CC specific stable traits for such characteristics as height,
CC seed and forage quality and maturity.

SQ Sequence 1814 BP; 530 A; 354 C; 415 G; 515 T;
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Best Local S
Matches 504
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(NOVS ) NOVARTIS AG.
De Vries SC, Hecht VFG,
WPI; 98-086529/08.
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03-AUG-1998
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                                                                                                                                                                                                                                                                             TGCAAGTCGCAACGGATACTTTTAGT-----ACCATACTTGGAAGAGGTGGATTTGGTA
                                                                                                                                                                                                                                                                                                                                       CAGCTGAAGAGGACCCAGAAGTGCACCTTGGTCAACTGAAGAGGTTTTCTCTGCGAGAAT
                                                                                                                                                        AACGAACACCAGGTGGTGAGCTGCAGTTTCAAACAGAGGTGGAAATGATTAGCATGGCTG
ttaaacatcttgtgctctctctcaattactttgacgtgaagtgttttttcatgttttcct
                                              tgtatccttacatggccaatggaagtgttgcttcgtgtctcagaggtaaaaactaaacaa
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llarity 64.6%;
Conservative
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Pred. No. 7.6e-52;
0; Mismatches 157;
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gtcacaacctccgcttgattggccaacgcggaagagaatcgcgctaggctcagctcgagg TCTTCTGTTCTATGACTATTTGGAAAATGGTAGCCTCTGGGATCTTCTTCATGGCCCTAC Query Match
Best Local Similarity
Matches 207; Conserv

Conservative

0;

Score 108; DB 1; Pred. No. 3.8e-15;); Mismatches 165

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                                       DNA encoding plant morphogenesis regulatory protein - useful to yield plants with short stems or altered inflorescence Claim 1; Pages 6-10; 17pp; Japanese.

The present sequence encodes an Arabidopsis thaliana plant morphogenesis regulatory protein (MRP), which can be used to yie a plant with, e.g. short stems or altered inflorescence. The MRF acts on a plant at a specific site for a specific period, and car therefore be used to regulate extraneous gene expression in a plant. The MRP's cDNA or genomic DNA can be used to transform a plant to increase its MRP expression, and therefore control the form (particularly stem length) of the plant.

Sequence 3176 BP; 927 A; 654 C; 659 G; 936 T;
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Arabidopsis thaliana plant morphogenesis regulatory protein
Plant; morphogenesis; regulation; short; stem; alteration;
inflorescence; extraneous; gene; expression; transformation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T62124 standard;
T62124;
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24-AUG-1995; JP-216187.
(MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KEN
(CHLK-) ZH CHLKYU KANKYO SANGYO GIJITSU
WPI; 97-206629/19.
                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana.
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/note=
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                                                                                                                                                                                                                                                                                                                                 "plant morphogenesis
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                                                                                                                                                                                                                                                                                                                                                                                                        expression;
ds.
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Length 3176
                                                                                                                 and can
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MRP
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/*tag= r 35873655 /*tag= s	i.	i.,	'n	·w	i.,	i	3041. 3118	29693040 /*tag=_k	28792968 /*tag= j				2+00: .233 /*tag= f	٠.	**************************************	**************************************		/*tag= a /*tag= 18822227	Location/Qualifiers	ol; form; length; liana.	ness; regulation; short; stem; alteration; extraneous; gene; expression; transformation;	irst entry) liana plant morpho	.rd; DNA; 9295 BP.			Page 1004	į		+070++070-++ 10	II IIII I	tegateacateac				
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24-AUG-1995; ; ; 24-AUG-1995; ; ; (MITS-) MITSU:	382-A -1997		intron	exon	intron	intron	e kon		exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	intron
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Matches 186
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30-DEC-1998; U13100.
24-JUN-1997; US-881706.
(SALK ) SALK INST BIOLOG
Chory J. L1 J.
WPI; 99-081275/07.
P-PSDB; W97819.
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Sequence 9295 BP; 2873 A; 1581 C; 1602 G; 3239 T;
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The present sequence encodes an Arabidopsis thaliana
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New receptor kinase Binl involved in brassinolide signalling - useful for promoting increased yield and disease resistance in plants and for modulating occyte maturation. Claim 8; Page 49-52; 72pp; English. This DNA sequence codes for a novel plant steroid receptor kinase, designated Binl (see W97819), which is involved in the pathway for the synthesis of the plant steroid hormone, brassinolide. 18 New
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Best Local Sim
Matches 175;
                                                                                                     Zea mays.
Zea mays.
W09909151-A2.
W09909151-A2.
25-FEB-1999.
17-JUL-1998; U14841.
13-AUG-1997; US-910386.
(REGC ) UNIV CALIFORNIA.
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Sequence 4104 BP; 1061 A; 870 C; 930 G; 1243 T;
                New RRK polynucleotides and nucleic acid constructs generating transgenic plants resistant to Xanthomonas Claim 12; Page 58-59; 67pp; English.
This invention describes a method for conferring disea
                                                                                                                                                                                                                                                   17-JUN-1999 (first entry)
Maize Xa21 gene DT4 cDNA fragment.
                                                                                                                                                                                                                       plant
                                                                                                                                                                                                                                         Xa21;
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99-204431/17.
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Pred. No. 1.6e-10;
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genes an
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   and
                 resistance
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New apoptosis-resistant virus-sensitive cell

Example 1; Page 38-41; 51pp; English.

The present invention describes an apoptosis-resistant virus-sensitive cell line into which an apoptosis resistance gene has been introduced.

The present invention describes an apoptosis-resistance gene has been introduced.

The recombinant viruses generated are capable of expressing apoptosis-associated genes. These can then be used in a variety of diseases for which the induction of apoptosis by gene transfer, or where the induction of harmful apoptosis, is therapeutic. The recombinant viruses are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an ademovirus vector capable of the reguired to induce cell death by apoptosis is shorter than that cells, required to replicate and produce the virus, resulting in failure to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Ma
Best Loc
Matches
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18-MAR-1999:
07-SEP-1998; J04010.
08-SEP-1997; JP-259235.
(RPRG-) RPR GENCELL ASIA F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                belonging to the Oryza longistaminata and Oryza sativa receptor Kinase-like protein (RRK) Xa21 multigene family. Such genes from cassava, maize and tomato are also described. The genes and proteins cabe used for enhancing resistance to Xanthomonas in a plant, preferably rice or tomato.

Sequence 3045 BP; 717 A; 739 C; 744 G; 735 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Base sequence of the plasmid pRx-ires-bsr.

Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer; autoimmune disease; graft rejection reaction; inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cowpox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUN-1999
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Pred. No. 1.7e
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1.7e-09;
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Sequence 6644 BP; 2166 A; 1573 C; 1424 G; 1481 T;
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                                                                                                                           25-JUN-1999 (first entry)
Base sequence of the plasmid pRx-Bcl-xl-bsr.
COMPOX virus; bsr; viral vector; expression;
crmA; bcl-z; bcl-xl; FLIP; survivin; IAP; ILP
autoimmune disease; graft rejection reaction;
inflammatory disease; ss.
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X33182 standard;
X33182;
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18-MAR-1999. 07-SEP-1998;

Homo sapiens. W09913073-A2. Synthetic.

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Combined the present invention describes an apoptosis-resistant virus-sensitive cell line into which an apoptosis resistance gene has been introduced. Combined the induction of apoptosis are capable of expressing apoptosis-sassociated genes. These can then be used in a variety of diseases for which the induction of apoptosis by gene transfer, or where the combinant viruses generated are capable of expressing apoptosis-sare useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of cutolimune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have concountered the problem where if an adenovirus vector capable of expressing an apoptosis-associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of contain a recombinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the base sequence of the cuts used in an example from the present invention.

Sequence 7372 BP; 2353 A; 1749 C; 1649 G; 1621 T;
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Hamada H;
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                                                                                            tgtaaaggcatgttctttgggttgaaaagctgggttatttgatatcttaagattgatgtt
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Example 1; Page 34-38; 51pp; English.

CC cell line into which an apoptosis resistant virus-sensitive cell line into which an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis. The recombinant viruses generated are capable of expressing apoptosis. CC associated genes. These can then be used in a variety of diseases for which the induction of apoptosis by gene transfer, or where the combinant viruses generated are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction through for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an adenovirus vector capable of cexpressing an apoptosis-associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis resistant dead gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the prosent sequence represent invention.

Sequence 7797 BP; 2542 A; 1760 C; 1656 G; 1839 T;
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Best Local S
Matches 291
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07-SEP-1998; J04010.
08-SEP-1997; JP-259235.
(RPRG-) RPR GENCELL ASIA F
Hamada H;
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Cowpox virus bsr full length gene sequence.
Cowpox virus; bsr; viral vector; expression; apoptosis; resistance;
Compox virus; bsr; viral vector; expression; apoptosis; resistance;
crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer;
autoimmune disease; graft rejection reaction; inflammation;
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hes 291;
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                              cgaatcattcactgtggcttgcttctgctaatttggaaggttcgtggttactcaattact
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Pred. No. 3.3e-09;
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                                                                                                                                           cell line into which an apoptosis resistance gene has been introduced.

Comparison of the recombinant viruses generated are capable of expressing apoptosis-
compared to the induction of apoptosis by gene transfer, or where the
comparison of harmful apoptosis by gene transfer, or where the
comparison of harmful apoptosis by gene transfer, or where the
comparison of harmful apoptosis by gene transfer, or where the
comparison of harmful apoptosis by gene transfer, or where the
comparison of harmful apoptosis by gene transfer, or where the
comparison of the virus for gene therapy which can be applied to cancer
comparison of the virus and graft rejection reaction, and apoptosis induction
comparison of the virus where if an adenovirus vector capable of
comparison of the virus will be destroyed because the period of
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So sequence 7996 BP; 2463 A; 2015 C; 1829 G; 1689 T;
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07-SEP-1998; J04010.
08-SEP-1997; JP-259235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New apoptosis-resistant virus-sensitive cell Example 3; Page 46-49; 5lpp; English.
The present invention describes an apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RPRG-) RPR GENCELL ASIA PACIFIC INC Hamada H;
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Pred. No. 3.4e-
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    Wang G;
WPI; 99-204431/17.
P-PSDB; W23533.
                                                   P-PSDB; W23533.

New RRK polynucleotides and nucleic acid constructs - generating transgenic plants resistant to Xanthomonas Claim 14; Page 61-62; 67pp; English.

This invention describes a method for conferring diserning invention describes the use of novel generation.
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This invention describes a method for conferring disease resistance in plants. The invention describes the use of novel genes and proteins belonging to the Oryza longistaminata and Oryza sativa receptor kinase-like protein (RRK) Xa2l multigene family. Such genes from cassava, maize and tomato are also described. The genes and proteins can be used for enhancing resistance to Xanthomonas in a plant, preferably in
                                                                                                                                                                                                                                         17-JUN-1999 (first entry)
Tomato Xa21 clone TRK2 DNA fragment.
Xa21; receptor kinase-like protein; plant disease resistance; cassava; m
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13-AUG-1997; US-910386.
(REGC) UNIV CALIFORNIA.
Hulbert SH, Richter T, R
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WO9909151-A2.
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                                                                                                                                                     T, Ronald
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cassava; maize; tomato; Xanthomonas; ss.
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20-NCV-1997:
13-MAY-1997: E02443.
14-MAY-1996: GB-010044.
10-WS ) NOVARTIS AG.
(NOVS ) NOVARTIS AG.
DE VT1es SC, Hecht VFG, Schmidt EDL, V&
WPI, 98-086529/08.
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                                                                                                                                                                                                               Production of apomictic seeds - useful in plant breeding Claim 28; Pages 75-77; 123pp; English.
The sequence is that of an EST clone showing high homology SERK LRR (leucine-rich repeat) sequences.
Sequence 981 BP; 286 A; 236 C; 180 G; 279 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                   V06587 standard; cDNA to mRNA; 981 BP. V06587; V06587; O3-ANG-1998 (first entry) Arabidopsis thaliana SERK LRR homologous EST receptor Kinase; apomixis; apomictic; seeds; plant breeding; leucine-rich repeat; ss. Arabidopsis thaliana.
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                                                                CCGCGTCACTCGTGGA 330
                       cagtgtcataagagtgta
                                                  CTGGGATCCAACTCTTGTTAATCCTTGTACCTGGTTCCATGTCACCTGTAACCAAGACAA
                                                                                                   AGGAGATGCTCTACGCTCTTCGCCGGAGTTTGACAGATCCAGACCATGTCCTCCAGAG
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/note= "shows
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; Pred. No. 1.5e.
0; Mismatches
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Pred. No. 2.5e-07;
0; Mismatches 41,
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1.5e-08;
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Search completed: June 23, Job time: 40529 sec
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03-AUG-1998 (first entry)
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous ES
receptor kinase; apomixis; apomictic; seeds
plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
Arabidopsis thaliana.
Key
CDS
142. .798
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20-W07-1997; E02443.
13-MAY-1996; GB-010044.
(NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS AG.
De Vries SC, Hecht VFG, Schmidt ED
WPI; 98-086529/08.
P-PSDB; W47018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Production of apomictic seeds - useful in plant breeding Claim 28; Pages 71-73; 123pp; English.
The sequence is that of an EST close showing high homology SERK LER (Leucine-rich repeat) sequences.
Sequence 1106 BP; 331 A; 258 C; 206 G; 311 T;
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Pred. No. 2.6e
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Maximum DB
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                            55.4
53.2
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1: /cgn2_6/ptodata/.

2: /cgn2_6/ptodata/.

3: /cgn2_6/ptodata/.

4: /cgn2_6/ptodata/.

5: /cgn2_6/ptodata/.

6: /cgn2_6/ptodata/.

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Copyright (c) 1993 - 2000 Compugen
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/6COMB.seq:*
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US-08-232-463-14
US-08-587-680A-24
US-08-447-185-3
US-08-447-185-3
US-08-447-185-3
US-07-717-331F-4
US-08-628-417-6
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US-08-628-417-6
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US-09-056-075-1
PCT-US96-03916-1
PCT-US96-03916-1
PCT-US96-03916-5
US-08-553-619B-8
US-07-820-011A-3
PCT-US93-00445-3
US-08-487-826B-13
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1934.536 Million cell updates/sec
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            Sequence 14, Appl
Sequence 21, Appli
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US-08-238-163-1	PCT-US93-06251-29	US-08-306-691B-15	US-08-030-096-5	US-08-567-375-15	US-08-186-222-1	US-08-764-100-9	US-08-764-100-13	PCT-US95-07753-3	PCT-US94-12364-24	US-08-331-355A-24	US-08-384-556A-3	US-08-046-583-12	US-08-644-271-2	US-08-374-834-2	PCT-US95-08493-20	PCT-US95-08493-18	PCT-US95-08493-1
Sequence 1, Appli	Sequence 29, Appl	Sequence 15, Appl	Sequence 5, Appli	Sequence 15, Appl	Sequence 1, Appli	Sequence 9, Appli	Sequence 13, Appl	Sequence 3, Appli	Sequence 24, Appl	Sequence 24, Appl	Sequence 3, Appli	Sequence 12, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 20, Appl	Sequence 18, Appl	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-08-232-463-14
US-08-232-463-14
                                                                 TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 7216 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Appli
Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: DORNER, F.

APPLICANT: SCHEIFLINGER, F.

APPLICANT: FALKNER, F. G.

TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: VA
COUNTRY: USA
ZIP: 22313-0299
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/07/9
APPLICATION NUMBER: EP 91:
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29.761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)683-4109
                                 IMMEDIATE SOURCE:
CLONE: pTZgpt-
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CITY: Alexandria
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US-08-587-680A-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vequence 24, Application US/08587680A Patent No. 5977434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Ronald
                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1431
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                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                               APPLICATION NUMBER: US/08/587,680A FILING DATE: 17-JAN-1996
                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
APPLICATION NUMBER:
                                     FILING DATE:
                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834
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               APPLICATION DATA:
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Song, Wen-Yuang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ronald, Pamela C.
                                   07-JUN-1995
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                                                     US 08/475,891
US 60/004,645
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                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Patent No.
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Best Local Similarity
Matches 165; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 576-030 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
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                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                             APPLICANT: Meyerowitz, Elliot | APPLICANT: Clark, Steven E. APPLICANT: Williams, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1282 GA 1283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pair
                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                            TITLE OF INVENTION: Plant Clavatal Nucleic & TITLE OF INVENTION: Transformed Plants, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4080 ga 4081
                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                              CITY: San Francisco
                                                                                                             COUNTRY:
                                                                                                                                STATE:
                                                                                                                                                                                    ADDRESSEE:
                                                                                         ZIP: 94111-4187
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                                                                                                                                California
                                                                                                                                                                                                                                                                                                                                                                         Application US/08473553A
                                                                                                                                                                  E: Flehr, Hohbach,
Four Embarcadero C
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                                                                                                                                                                                                                                                                                                                   Meyerowitz, Elliot M
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                                                                                                             United States
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Center,
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Pred. No. 1.2e-08;
0; Mismatches 134
                                                                                                                                                                      Albritton & Herbert
Suite 3400
   Version #1.30
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; LOCATION:
US-08-473-553A-1
                                                                                                                                                                                                                                                                                    RESULT 4
US-08-447-185-2
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                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Tanksley,
APPLICANT: Martin, G
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 133; Conserv
                                                                                                                                                                                                                                    Sequence 2, Application US/08447185
Patent No. 5648599
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                      NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael L. Goldman
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4793 AAGGTGGTCATCTTCAATGGGAGACGAGACATAGAGTAGCCGTGGAAGCTGCAAAGGGCT 4852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4733 ATCTCCTTCTTTATGAGTACATGCCTAATGGAAGCCTTTGGAGAGCTTTTGCATGGATCTA 4792
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-
                                                                                                STREET:
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                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                   TAGTTGAT 4980
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                                                   14603
                                                                                                Rochester
                                                                               New York
                                                                U.S.A.
                                                                                                                                                             Tanksley, Steven D.

MARTTIN, Gregory B.

PANTION: GENE CONFERRING DISEASE RESISTANCE

ZENTION: TO PLANTS BY RESPONDING TO AN AVIRULENCE GENE IN PLANT PATHOGI

ZQUENCES: 5
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Pred. No. 1.8e-06;
0; Mismatches 115
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; TOPOLOGY: un ; MOLECULE TYPE: US-08-447-185-2
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Sequence 3, Application US/08447185
Patent No. 5648599
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.5%;
Best Local Similarity 53.4%;
Matches 149; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Goldman Mr., Michael L. TELECOMMUNICATION INFORMATION:
                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                     APPLICANT: Tanksley, Steven D.

APPLICANT: MATTIN, GREGORY B.

TITLE OF INVESTION: GENE CONFERRING DISEASE RESISTANCE

TITLE OF INVESTION: TO PLANTS BY RESPONDING TO AN AVIRULENCE GENE IN PLANT PATH

NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3407 gaggtgggtttgggaaagtctacaagggacgcttggcagacggaactcttgttgctgtca 3466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CURRENT APPLICATION DATA:
             SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                     CITY: Roche
STATE: New
COUNTRY: U.
ZIP: 14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 ATGAGATGATTCTAATTTATAAATACATGGAGAATGGGA 361
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                              New York
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US/08/447,185
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Pred. No. 8.1e-06;
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RESULT 6
US-07-717-331F-9
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SEQUENCE CHARACTERISTICS:
LENGTH: 2443 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/07717331F Patent No. 5484905 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.5%;
Best Local Similarity 53.4%;
Matches 149; Conservative
          COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/717,331F
FILING DATE: June 19th 1991
CLASSIFICATION: 800
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NAME: GOLdman Mr., Michael L.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)263-1000
TELEFAX: (716)-263-1600
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                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua APPLICANT: Stein
TITLE OF INVENTION: A Receptor Protein Kinase Gene
TITLE OF INVENTION: Encoded At The Self-Incompatability Locus
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APPLICATION NUMBER: US/08/111,078
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                          STREET: Trumbull
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                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                          Connecticut
                                                                                                                                                                                                                                                                                               25 Skytop Drive
                                                                                                                                                                                                                                                                                                                       Yahwak & Associates
                                                                                                                                                                    Floppy Disk
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Pred. No. 1.3e-05;
0; Mismatches 127;
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 9:
               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/717
FILING DATE: June 19th 1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2159 TTCTTGA 2165
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua APPLICANT: Stein
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                      STREET: Trumbull
                                                                                                                                                COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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25 Skytop Drive
                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                A Receptor Protein Kinase Gene 
Encoded At The Self-Incompatability Locus
                                                                                                              US/07/717,331F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 59; DB 1; Le
Pred. No. 2.1e-05;
0; Mismatches 145;
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TELEPHONE:

(203)268-1951

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US-07-717-331F-4
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2833 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/07717331F Patent No. 5484905
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Best Local Similarity
        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/717,331F
FILING DATE: June 19th 1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION INFORMATION:
TELEPHONE: (203)268-1951
TELEPHONE: (203)268-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: A Receptor Protein Kinase Gene
TITLE OF INVENTION: Encoded At The Self-Incompatability Locus
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4015 aatatototoaacoggaaaatottoagagaaaacogacgttttoggataoggaatoatgo 4074
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                                                                                                                                                                                                                                                                                          06611
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(203)268-1951
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2.2e-05;
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; STRANDEDNESS: single
; TOPOLOGY: Linear
; MOLECULE TYPE: DNA
US-07-717-331F-4
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Best Local S
Matches 141
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COUNTRY:
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: FOR PC CONS/MS-DOS
COUNTRY: FOR PC-DOS/MS-DOS
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                                             FILING DATE:
APPLICATION NUMBER: US 07/847,564
EILING DATE: 03-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: POCHOPIEN Ph.D., Donald J.
REGISTRATION NUMBER: 32,167
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 107-8889
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rothstein, Steven J.
APPLICANT: Goring, Daphne
TITLE OF INVENTION: S-LOCUS RECEPTOR KINASE GENE IN A
TITLE OF INVENTION: SELF-INCOMPATIBLE BRASSICA NAPUS LINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08265628
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                                     312-707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McAndrews, Held &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4%;
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Pred. No. 0.00017;
0; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Malloy, Ltd
Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version
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US-08-487-826B-13/c
                                                                                                                                                                                                                                       Sequence 13, Application US/08487826B Patent No. 5993827 GENERAL INFORMATION:
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Best Local Similarity 50.8%;
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    APPLICANT: Sim, Kim L.

APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, xin-zhaun
APPLICANT: Su, xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERVTHROCYTE BINDING PROTEINS
TITLE OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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LOCATION: 1..2574

LOCATION INFORMATION:

PUBLICATION INFORMATION:

AUTHORS: GORING, DAPHNE

AUTHORS: ROTHSTEIN, STEVEN J.

TITLE: ROTHSTEIN, STEVEN J.

TITLE: S-LOCUS RECEPTOR KINASE GENE IN A

TITLE: FUNCTIONAL SERINE/THREONINE KINASE

RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 2749
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LENGTH: 2749 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OKGANISM: Brassica napus
STRAIN: oleifera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                TTCTTGA 2168
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Newport Center Drive
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Pred. No. 0.00034;
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Bear
16th
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RESULT 11
US-08-628-417-6/c
US-08-628-417-6/c
; Sequence 6, Application US/0862841
; Patent NO. 5627054
; GENERAL INFORMATION:
; APPLICANT: GILLESPIE, DAVID
; TITLE OF INVENTION: COMPETITO!
; TITLE OF INVENTION: POLYMERAS!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: (
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-487-826B-13
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TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.3%;
Best Local Similarity 48.1%;
Matches 180; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1456
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                tgtctgcattttgatttatgaaaattgttgttgttctttgtatttgtaagatttagtggc 1515
                                                                                                                                                                                                                                                                                                                                                                                 tagtactttgaatacactgttttgcttttcttgttcagatcaactttgtatattgtaaag 1575
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N: 435
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235-0176
                                                                                   US/08628417
     COMPETITOR PRIMER ASYMMETRIC POLYMERASE CHAIN REACTION
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US-08-628-417-6
                                                                                                                                                                                                 Sequence 3, Patent No. 5
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Best Local Similarity 50.2%;
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REFERENCE/DOCKET NUMBER: DAN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-671-1158
TELEFAX: 410-671-2534
INFORMATION FOR SEQ ID NO: 6:
                                                                                                         GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: BIFFONI, ULYSSES J
REGISTRATION NUMBER: 39,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1461 gcattttgatttatgaaaattgttgttgttctttgtatttgtaagatttagtggctagta 1520
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: OF
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                                                      TITLE OF INVENTION: Procedures and Materials for TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                              1521 ctttgaatacactgttttgcttttcttgttcagatcaactttgtatattgtaaaggcatg 1580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL ADDRESSEE: DEFENSE COMMAND STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC) CITY: ABERDEEN PROVING GROUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                           59
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                         TTTTTTTTTTTTTTTTTTAGTAAAATTATTTCTAAAGTTTTATTGTCTTTATC 5
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                                                                                                                                                                                                                  Application US/08567375
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                                                                                                                                                                Ronald, Pamela C.
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Pred. No. 0.004;
0; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 240;
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                                                                                          Conferring
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WESULT 13
US-08-587-680A-3
; Sequence 3, Application US/08587680A
; Patent No. 5977434
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REGISTRATION NUMBER: 34,774

REFERENCE/OCCKET NUMBER: 0230

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAC: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3921 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 120; Conserv
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLIAGE 29-SEF FILING DATE: 29-SEF FILING DATE: 29-SEF FRIOR APPLICATION NUMBER: US 08/475,891
APPLICATION NUMBER: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 07-JUN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                1234
                                                                                                                                                                                                                                                                                             1174
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                                                                                                                                                                           2354 tac 2356
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: join(1..2676, 3520..3918)
OTHER INFORMATION: /product- "Xa-21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                TTCAGAGGGTCTCTTCCATCATCGTTGGGCAGGCTTAAAAACTTAGGCATTCTACTCGCC 1293
                                                                                                                                                                                                                                                  ttctccggtcctattccggaatcattgggaaagctttcaaagctgagatttctgtgagta 2353
                                                                                                                                                                                                                                                                                             ATTCCGAAGGATATTGGCAATCTTATTGGCTTACAACATCTCTATCTCTGCAACAACAAT 1233
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: California
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Pred. No. 0.041;
0; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3921;
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Ronald, Pamela C.

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; NAME/KEY: CDS
; LOCATION: Join(1..2676, 3520..3918)
; OTHER INFORMATION: /product= "xa-21"
US-08-587-680A-3
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Best Local Similarity
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                                                                                                                  1114
                                                                                                                                                        2174
                                                                                                                                                                                            1054 AAATTACAAACATTGAACTTGGGAGAAAATAACCTGGGGGGAGTTCTTCCTAATTCGTTT 1113
                                                                                                                                                                                                                   2114 acamaaccamatccamgatitgacagamgamgcactggmgttmccttttgtmattgmamtc 2173
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LENGTH: 3921 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-UUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 00
FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 00
APPLICATION NUMBER: US 00
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08
FILING DATE: 17-JAN-1996
CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                TCCAATCTTTCCACTTCGCTTAGTTTTCTTGCACTTGAATTGAATAAGATCACAGGAAGC 1173
                                                                                                                                                    tttttaacaagtttcttattttcttacagggagctttacagtaacaacataactggcccg 2233
ttctccggtcctattccggaatcattgggaaagctttcaaagctgagatttctgtgagta 2353
                                        ATTCCGAAGGATATTGGCCAATCTTATTGGCCTTACAACATCTCTATCTCTGCAACAACAAT 1233
                                                                        attectagtaatettggaaatetgaeaaaettagtgagtttggatetttaettaaaeage 2293
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Song, Wen-Yuang
Szabo, Veronique
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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04-DEC-1995
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                                                                                                                                                                                                                                                                                         1.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                       Score 46.2; DB 4; Length 3921; Pred. No. 0.041;
                                                                                                                                                                                                                                                                         Mismatches
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US-08-475-891A-3
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                                                                                                                                  Matches
                                                                                                                                                    Best
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING LALL.
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
APPLICATION TO THE TOTAL PROPERTY NAME: 17-JAN-1995
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ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 06-JUN-199
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MEDIUM TYPE: Floppy disk
                      2174 tttttaacaagtttcttattttcttacagggagctttacagtaacaacataactggcccg 2233
                                                                                       2114 acaaaacaaatccaagatttgacagaagaagcactggagttaccttttgtaattgaaatc 2173
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                                                                 1565 AAATTACAAACATTGAACTTGGGAGAAAATAACCTGGGGGGAGTTCTTCCTAATTCGTTT 1624
                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: Join(512.
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                 Local Similarity
nes 120; Conserv
                                                                                                                                                                                                                                   OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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Song, Wen-Yuang
                                                                                                                                  Conservative
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                                                                                                                                                                                                                               join(512..3149, 3993..4393)
RMATION: /product= "RRK-B"
RMATION: /note= "Xa21 Xanthomonas spp. disease
RMATION: resistance gene RRK-B from rice (Oryza
RMATION: sativa)"
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                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                  1.18;
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                                                                                                                                 Score 46.2; DB 3;
Pred. No. 0.051;
0; Mismatches 123;
                                                                                                                                                                Length 5992;
                                                                                                                                  Indels
                                                                                                                                  0
                                                                                                                                  Gaps
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COMPUTER: IBM PC PU 1008

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

CORRENT APPLICATION DATA:

APPLICATION UNMEER: US/08/475,891A

FILING DATE: 05-JUN-1995

CLASSIFICATION UNMEER: US 08/373,375

FILING DATE: 17-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bastlan, Kevin L.

REGISTRATION NUMBER: 34,774

REGISTRATION NUMBER: 34,774

REFERENCE/DOCKET NUMBER: 02370-058910US

TELEPHONE: (415) 576-0200

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARROTERISTICS:

LENGTH: 6256 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FOLECILE TYPE: Data
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US-08-475-891A-1
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                                            Query Match
Best Local Similarity
Matches 120; Conserv
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APPLICANT: Wang, Guo-Liang
APPLICANT: Wang, Guo-Liang
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
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2114 acaaaacaaatccaagatttgacagaagaagcactggagttaccttttgtaattgaaatc 2173
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                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                NAME/KEY: CDS
LOCATION: Join(1648..4383, 5178..5513)
OTHER INFORMATION: /product= "RRK-F"
OTHER INFORMATION: /note= "%xa21 %anthomonas spp. disease
OTHER INFORMATION: resistance gene RRK-F from rice (Oryza
OTHER INFORMATION: sativa)"
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STATE: California
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ilarity 49.48;
Conservative
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                                            Score 46.2; DB 3; Length 6; Pred. No. 0.052; O; Mismatches 123; Indels
                                                                                       Length 6256;
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2962 TAC 2964
                                                                                                2902 TTCAGAGGGTCACTTCCATCATCGTTGGGCAGGCTTAGAAACTTAGGCATTCTAGTCGCC 2961
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Search completed: June 23, 2000, 22:44:24 Job time: 40210 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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SOURCE
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B09168 B09168.1 GI:2090299 GSS. thale cress.
                                                                                             Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
BAC End Sequences at ATGC Unpublished (1997) Other_GSSs: T2E10-Sp6
                                                      Arabidopsis.
1 (bases 1 to 1202)
Feng, J., Dewar, K., B
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AI729340 BNLGH1933
AL093535 Arabidops
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AU15634 AG87p6ou
T45280 8543 Lambda
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AI728030 BNLGH1962
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AW234133 sf34f03, y
C22657 C22657 Rice
AW257240 EET305377
AI729170 BNLGH1128
AW201545 sf04d10, y
C22693 C22693 Rice
AU367518 660013E08
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A0969360 LERNM53TF
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A1486453 EST3244774
AA738544 SDRLK2 SO
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  NGTTATCCTTAACATGCTAAGGGAAATGTCGCTTCTTGTTTGA 702
                                                         TTCACAGATATCTCCTCAGGCTACNTCGGTTCTGTATGAACCCTTACCGAAAGAATGCTT
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Class: BAC ends
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High quality se
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Fax: 215-898-8780
Email: jecker@atge
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University of Pennsylvania
Dept. of Biology, University of Pe
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="T2E10"
/clone_lib="TAMU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Termaphrodite"
/note="Vector: BeloBACII; Site_1: HindIII; Site_2:
HindIII; Produced by Rod Wing"
275 c 238 g 354 t 13 others
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Pred. No. 4.4e-39;
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 ATCTATATACTATGCAGAGATTAAACCCGGGGATCCAGTTCTGGATTGGTTCAGGAGGAA
                ttacactaatgacacagagaggccaccgtcacaacctccgcttgattggccaacgcgggaa 3802
                                                                                                                          TAAGTGTTGCATATTGCTTAAGAGGTAAAAAAAAGGAACATAA-----
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Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utter Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based polymorphisms
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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For addtional information,
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sheared to 0.4~0.7 Kbp before ligation."
177 c 112 g 220 t
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/strain="Landsberg erecta"
/db_xref="taxon:3702"
/clone="LERJM53"
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                                                             -GCTATAAACTTTTGATTTCAGGAGTTTAAGATTTTGTG
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Pred. No. le-34;
0; Mismatches 2
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 CGGATGGCACCAAAATCGCTGTAAAAAGATTGACTGATTTTGAACGTCCAGGAGGAGATG
                            cagacggaactcttgttgctgtcaagagactgaaggaagagcgaactccaggtggagagc
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Tel: 301 838 0200
Fax: 301 838 0208
Email: at@tlgr.org
For additional information, s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; eudicotyledons; core euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utter
Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of
Arabidopsis thaliana and identification of sequence-based
                                                                                                                                                                                                                                                                                                                                                                                                                                      On Dec 15, 1999 this sequence version Contact: Xiaoying Lin
The Institute for Genomic Research
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Class: shotgun.
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                                                                                                                                                           /clone_lib="LERG"
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102 c 154 g 173 t 1 others
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/clone="LERJM53"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core

eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
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                                                      Unpublished (1999)
On Feb 18, 1999 this sequence version replaced gi:4297707.
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                    1 (bases 1 to 532)

Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,

Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Kucaba, T., Martin, J.,

Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,

Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,

Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,

Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
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AW233982.1 GI:6566309
EST.
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                        314 286 1800
314 286 1810
      est@watson.wustl.edu
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Conservative

4.78;

Score 192.8; DB 7 Pred. No. 1.7e-30; Mismatches

DB 79;

Length

0,

Gaps

0

3997

342

3937

282

222

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This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com High quality sequence stop: 403.
/clone="GENOME SYSTEMS CLONE ID: /clone_lib="Gm-cl028"
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Glycine max"
/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                                                     /tissue_type="roots of 'Supernod'
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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TGGATATGGTGTGATGCTTCTTGA

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REFERENCE
AUTHORS
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                                                                                                                                                                     130 AATACCTACATGAACACTGTAATCCAAAGATTATTCACCGTGATGTTAAAGCAGCTAATG
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                                                                                                                                                                                                                                                                                                       Match 4.28;
Local Similarity 72.08;
aatatctctcaaccggaaaatcttcagagaaaaccgacgttttcggatacggaatcatgc
                                                                                                         actataaagacactcacgtgacaacagcagtccgtggcaccatcggtcacatcgctccag
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EST244774 tomato ovary,
CLED8G2, mRNA sequence.
AI486453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On May 7, 1998 this sequence version replaced Contact: David Frisch Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujil,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter, Martin,G.B., Tanksley,S.D. and Giovannoni,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clemson University
100 Jordan Hall, Clemson, SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI486453.1
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864 656 4293
1: dfrisch@CLEMSON.EDU.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                   respectively.
                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; cLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector Lamda ZAP II with 5 and 3' ends located at the EcoRI and XhoI sites,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="tomato ovary, TAMU"
/tissue_type="carpel"
/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XL1-Blue MRF/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Lycopersicon
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cleD8G2"
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                          ggtggagagctccagtttcaaacagaagtagagatgataagtatggcagttcatcgaaac 3552
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                                                                                       GGAGCACTTCCAGATGGCACTAAGATTGCTGTAAAACGGTTAACTGATTACGAAAGTCCT
                                                                                                                      428;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Universitaetsstrasse 1, Tel: (49)-211-81-14953 Fax: (49)-211-81-14871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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Similarity 55.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: leaf; Vector: Lambda ZAP II; Site_1: Eco
Site_2: Xho I; leaf cDNA library from green leaves,
unidirectionally cloned"
194 c 293 g 251 t
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/clone="sbrLK2"
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/strain="cv. TX430"
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barrel medic.
Medicago truncatula
Medicago truncatula
Euxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Euxaryota; Viridiplantae; Streptophyta; eudicotyledons; core
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
euphyllophytes; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                                 Harrison, M.J., Liu, J., Gonzales, M.B.
ESTs from phosphate starved roots
Unpublished (1999)
On May 1, 1997 this sequence version
                                                                                                                                                                                                     Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK
Tel: 580-223-5810
Fax: 580-221-7380
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                                                                                                         Email: mjharrison@noble.org
Developmental stage: phosphate starved; Date: 01/23/00; Submitted
to the Database of Expressed Sequence Tags (dbEST) on 01/26/00;
More information is available at
'http://chrysie.tamu.edu/medicago'.
                                                                                                                                                                                                                                                                                                   Contact: Maria J. Harrison
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Contact:
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On Nov 29
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Annen, F., Chang, J.-L., Paterson, A.H. and Stockhaus, J.
Characterization of 14 different putative protein kinase clones of the C4 plant Sorghum bicolor Mol. Gen. Genet. 259 (1), 115-122 (1998)
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                         Tel: (49)-211-81-14953
Fax: (49)-211-81-14871
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stockha@uni-duesseldorf.de
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                                                                                                                                                                                                                               1 (bases 1 to 655)
Annen, F., Chang, J.-L., Paterson, A.H. and Stockhaus, J.
Characterization of 14 different putative protein kinase cDNA
clones of the C4 plant Sorghum bicolor
clones of the C4 plant Sorghum bicolor
Mol. Gen. Genet. 259 (1), 115-122 (1998)
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AA738546
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                                                                 Universitaetsstrasse 1,
Tel: (49)-211-81-14953
Fax: (49)-211-81-14871
                                                                                                       Heinrich-Heine-Universitaet maiversitaetsstrasse 1, 40225
                                                                                                                                                        Contact: Stockhaus J
Institut fuer Entwicklungsbiologie und
                                                                                                                                                                              On Jan 13, 1998 this sequence version replaced gi:3421471.
Contact: Stockhaus J
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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                                                stockha@uni-duesseldorf.
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/clone="sbRLK5"
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/strain="cv. TX430"
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lon/Qualifiers
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Pred. No. 8.1e-25;
0; Mismatches 77;
                  Error: 0.00
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                gatacggaatcatgcttctaga 4081
                                                                     gtcacatcgctccagaatatctctcaaccggaaaatcttcagagaaaaccgacgttttcg
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/strain="cv. TX430"
/db_xref="taxon:4558"
/clone="SbRLK4"
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Pred. No. 1.1e-24;
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                                  survey sequence.
B27171
B27171.1 GI:2513
GSS.
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EST.
Oryza sativa.
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p25047
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Contact: Yuzo Minobe
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 299)
Minobe, Y. and Sasaki, T.
Rice cDNA from root
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                                                                                B27171 464 bp I
T2E10TF TAMU Arabidopsis
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Fax: 0298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: minobe@rtcs0.riken.go.
PROJECT ='RGP'.
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/strain="%liponbare, sub_species Japonica"
/db_xref="ftaxon:4530"
/clone="R2976_lA"
/clone="htb="%rice root"
/clone_lib="%rice root"
/note="Prepared from seedling root. "
54 c 67 g 85 t
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 Embryophyta;
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R2976_1A, mRNA
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 Tracheophyta;
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3002 aatttgatttcaggtgggtatggtataactggagcaatagctggtggagttgctgcaggt 3061
                     agcgaactccaggtgg 3497
                                                                                                                                                                                                                                              CAGCCGAAGAGGACCCTGAGGTTCACTTGGGGCAGCTTAAGCGGTTCTCTCTACGGGAAC
                                                                                                                                                                                                                                                                  cagccgaagaagatccagaagttcatctgggacagctcaagaggttttctttgcgggagc 3361
                                                                                                                                                                                                                                                                                                                                                        gtcattgttttttaagttacaaactcttttgagtaaaatctcgattgcaaaatctctatg 3301
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                                                                                                  TTCAAGTAGCAACTGATAGCTTCAGCAACAAGAACATTTTGGGCCGAGGTGGGTTCGGAA
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                                                                            AAGTCTACAAATGCCGTCTTGCTGATGGAACACTTGTTGCAGTCAAACGGCTTAAAGAAG
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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Unpublished (1997)
Other_GSSs: T2E10TR
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Class: BAC ends
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eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Use of a BAC End Sequence
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Similarity 64.58;
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/sex="hermaphrodite"
/note="Vector: BeloBACII; Site_1:
/note="Vector: BeloBACII; Site_1:
/note="Vector: BeloBACII; Site_1:
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in 87 c 115 g 143 t
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="T2E10"
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Kelley,J.M., Field,C.E., Craven,M.B., Adams,M.D.
464
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Pred. No. 5.2e-23;
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BASE COUNT
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AUTHORS
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Best Local Similarity
Matches 210; Conserv
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acgaagaattcgaagcggttgttggagatttcgggttggcaaagctaatggactataaag 3963
                                                                                        acactcacgtgacaacagcagtccgtggcaccatcggtcacatcgctccagaatatctct 4023
                                                                    AGACATCTGTGGCTGCTCAGGTCCGTGGAACTATGGGTCACATTGCCCCCTGAATATTTGT
                                                                                                                                          ATGAAGGTTTTGAACCGGTTGTTGGTGATTTCGGCTTGGCCAAGCTGGTGGATGTACAGA 979
                                                                                                                                                                                                              1 (bases 1 to 1435)
Annen, F., Chang, J.-L., Paterson, A.H. and Stockhaus, J. Characterization of 14 different putative protein kinclones of the C4 plant Sorghum bicolor Mol. Gen. Genet. 259 (1), 115-122 (1998)
98409267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heinrich-Heine-Universitaet
Universitaetsstrasse 1, 40225 Duesseldorf,
Tel: (49)-211-81-14953
Fax: (49)-211-81-14871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Stockhaus J
Institut fuer Entwicklungsbiologie und
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euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
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AA738545.1 GI:3421470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: leaf; Vector: Lambda ZAP II; Site_1: Site_2: Xho I; leaf cDWA library from green leaves, unidirectionally cloned; cloned; 300 c 389 g 381 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Sorghum bicolor"
(strain="cv. TX430"
/db_xref="taxon:4558"
/clone="SbALK3"
/clone_lib="Sorghum bicolor cv. TX430 leaf"
/dev_stage="green"
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Pred. No. 5.3e-23
0; Mismatches 8
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                                     CAACGGGTCAATCGTCTGAAAAGACTGATGTGTTTTGGTT 553
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EST265720 tomato callus, T
CLEC14J5, mRNA sequence.
AI896277.1 GI:5602179
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Clemson University
100 Jordan Hall, Clemson, SC 29634, UK
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Generation of ESTs from tomato callus tissue
Unpublished (1999)
On May 18, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
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eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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/clone="clEC14J5"
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71.3%;
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Pred. No. 1e-21;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Ben Burr
Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 597)
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AI727837
AI727837.1 GI:5046689
EST.
AI729440 703 bp mRNA EST 11-JUN-1999
BNLGH113383 Six-day Cotton fiber Gossypium hirsutum cDNA 5' si
to (U93048) somatic embryogenesis receptor-like kinase [Daucus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: burr@bnlux1.bnl.gov
Seq primer: T3 Primer.
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ESTs from developing cotton fiber
Unpublished (1999)
On Jun 5, 198 this sequence version replaced g1:3187180
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Similarity 67.8%;
02; Conservative
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/clone_lib "Six day Cotton fiber"
/tissue_type "immature fiber"
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Pred. No. 2.5e
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                                                                                          CCACTGGGAAGTCATCAGAAAGAACGGATGTCTTTGGTTATGGGATTATGCTTCTAGA
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Tel: 516-344-3396
Fax: 516-344-3407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999 On Jun 5, 1998 th Contact: Ben Burr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gössypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 703)
Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.
ESTs from developing cotton fiber
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AI729440.1 GI:5048292
EST
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Seq primer: T3 Primer.
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nilarity 67.8%;
Conservative
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/note="Yector: pBluescript II KS+"
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/cultivar="Acala Maxxa"
/db_xref="taxon:3635"
/clone_lib="Six-day Cotton fiber"
/tissue_type="immature fiber"
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Pred. No. 2.5e-20;
0; Mismatches 96;
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Listing first 45 summaries
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Maximum DB seq length: 1000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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De,V.S., Schmidt,E.D., Van,H.G. a
PRODUCTION OF APOMICTIC SEED
Patent: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
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Sequence :
A67821
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De, V.S., Schmidt, E.D., Van, H.G. average production of APOMICTIC SEED Patent: WO 9743427-A 20-NOV-1997;
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1 (bases 1 to 894)
De, V.S., Schmidt, E.D., V
PRODUCTION OF APOMICTIC
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                                               TGTGTGGAACAATTCCAGTAGAAGGACCTTTTGAACACATTCCTATGCAAAACTTTGAGA
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                              CTTABAAAGAAGTTGAAGAACCTATAAAGAAGAA-TGTTAGGTGACCTTGTAAGAACTCT
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/db_xref="G1:4756646"
/db_xref="G1:4756646"
/translation="gp1QASEGDALHALRRSLSDPDNVVQSWDPTLVNPCTWFHVTCN
QHHQVTRLDLGNSNLSGHLVPBLGKLEHLQYLYGIITLLDFDYLKTFTLSVTHITECF
ESYSELYKNEIQGTIPSELGNLKSLISLDLYNNNLTGKIPSSLGKLKSLVFLRLNENR
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                                                                                 aaccaagaccaaccgcgtcactcgtgtggatttgggaaattcaaacctctctggacatctt 399
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aacaacaatcttacagggatagttcccactttcttgggaaaattgaagtctctggtcttt
                             ACTGGCCCGATTCCTAGTAATCTTGGAAATCTGACAAACTTAGTGAGTTTGGATCTTTAC
                                            caaggaactataccttccgaacttggaaatctgaagaatctcatcagcttggatctgtac 519
                                                                                                                                          AACAACGAGAACAGTGTCATAAGAGTTGATTTGGGGGAATGCAGAGTTATCTGGCCATTTA 449
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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LTNITIQVLDLSNNRLSGSVPDNGSFSLFTPISFANNLDLCGFVTSHPCFGSPPFSP
PPFFLQPPVSTPSGYSGTTGALAGGVAAGAALPFAAPAIAFAWWRRRSPLJEFDVPA
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PSQPPLDWPTRKRIALGSARGLSYLDHCDFWFIIHTDVFGYGIMLLELTITGQRAFDLA
KLMDYKDTHYTTAVRGTIGHLAPEYLSTGKSSEKTDVFGYGIMLLELTITGQRAFDLA
RLANDDDVMLLDWYKGLLKEKKLEMLYDPDLQTNYEERELEQVIQVALLCTGGSPMER
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/translation="MessyvpfillsbiillpnHslwlasanilegdalhtilrvtlydpn
NVLQSWDPTLYNPCTWFHYTCNNENSVIRVDLGNAELSGHLVPELGVLKNLQYLELYS
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195. .2072
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/db_xref="taxon:3702"
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                   aactccgaaggagatgctctctacgctcttcgccggagtttgacagatccagaccatgtc 282
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AACACTGAAGGTGACATACTGTACAAGCAAAGGTTGGCATGGGAGGACCCAAACAACGTG 140
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U62279
U62279.1 GI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (26-JUN-1996) John D. Hipskind, Botany Pathology, Purdue University, West Lafayette, IN Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hipskind, J.D., Nicholson, R.L. and Goldsbrough, P.B.
Isolation of a cDNA encoding a novel leucine-rich repeat motif
Sorghum bicolor inoculated with fungi
Mol. Plant Microbe Interact. 9 (9), 819-825 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
euphyllophy
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                                                                     Conservative
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                                                                                                                                                                                                                                                /protein_id="AAC49559.1"
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LTSLLESKLQENGLGGIPASLGNIKALOFSRLNDNMLTGTVPSKSFPLSTFGNLTEL
                                                                                                                                                                                                                                                                                                                                                                               /function="protein-protein ligand binding"
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glycoprotein; contains six N-glycosylation sites
[NX(S/T)]"
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                                                                                                                                                                               /evidence=not_experimental
232 c 207 g 250
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                                                                 Score 151.2; DB 8; pred. No. 3.1e-26; 0; Mismatches 153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACCTTCTTACCGGCGAAATCCCAACTACGCTTGGTTCTGTCAGCACGCTGCGATATCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (18-JAN-1996) P. Vera, Universidad Politecnica de Valencia, Inst. de Biologia Molecular y Celular de Piantas, de Vera 14, E- 46022 Valencia, SPAIN

2 (bases 1 to 4604)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
euphyllophytes; Solananae; Solanales; Solanaceae; Solanum; Potatoe;
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X95269
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                                                                                                                                                                   113. .4355
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join(113. .345,2381. .
4283. .4355)
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                                                                                                                                                                                                                                                       /tissue_type="leaf" <1. .345
                                                                                                                                                                                                                                                                                                       /organism-"Lycopersicon/cultivar-"VFN8"
                                                                                                                                                  /gene-"LRP"
                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                           /db_xref="taxon:4081"
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Query Match 8.7%;
Best Local Similarity 69.1%;
Matches 132; Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; eudhyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus. 1 (bases 1 to 1755) Schmidt, E.D., Guzzo, F., Toonen, M.A. and de Vries, S.C. A leucine-rich repeat containing receptor-like kinase marks somatic plant cells competent to form embryos Development 124 (10), 2049-2062 (1997)
                                                                                                                                                                  Daucus carota
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U93048.1 GI:2224910
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4283. .>4604
/number=6
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3153. .428
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2709. .292
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Pred. No. 3.7e-13;
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2 (bases 1 to 1755)
Schmidt,E.D.L., Guzzo,F., Toonen,M.A.J. and de Vries,S.C.
Direct Submission
Submitted (12-MAR-1997) Molecular Biology, Agricultural University
Submitted (12-MAR-1997) Molecular Biology, Agricultural University
                                                                                                   Mo//97 1815 bp DNA
Sequence 2 from Patent W09743427.
A67797
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Daucus carota
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                               carrot.
                                                                                    A67797.1
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/product="somatic embryogenesis receptor-like kinase"
/product="somatic embryogenesis receptor-like kinase"
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/proteain_id="AAB61708.1"
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/translation="MKRNSINILNYMOFTDAYLDKYGYLMTLELYSNNISGPIPSDEGIPTUGKLTRLRELAUNNSLSGPIPMSLINITTLOVLDL
SUNRLYSLDYLYNNSFSGPIPDTIGKLTRLRELAUNNSLSGPIPMSLINITTLOVLDL
SUNRLSGPVDDNGSFSLFTPISFANNLNLCGPVTGRPCPGSPPFSPPPPIPPSTVOP
PGQNGPTGAIAGGVAAGAALLFAAPAANFARKTREEFFDFAAEDDFEVHLGGLK
RFSLRELGVATDTFSTILGRGGFGKVVYKGRLADGSLVAVKRLKEERTPGGETLOFTER
RFSLRELGVATDTFSTILGRGGFGKVVXGRLADGSLVAVKRLKEERTPGGETLOFTER
REMINAVHRULLRIGGCMTFTERLLVYFYMANGSVASCLREBGDFSBPDLDWTTRKRI
EMISMANHRULLRIGGCMTFTERLLVYFYMANGSVASCLREBGDFSBPDLDWTTRKRI
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VRGTLGYIAPEYLSTGKSSEKTDVFGYGIMLLELITGGRAFDLARLANDDDYMLLDWV
KSLLKEKKLEMLYDDDLENNYIDTEVEQLIQVALLCTGGSPERFKMSEVYRMLEGDG
LAEKWDEWQKVEVIHQDVGLAPHRTSEMILDSTDNLHAFELSGPR"
1 347 c 407 g 495 t
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/db_xref="taxon:4039"
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52.1%;
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Pred. No. 3.5e-10;
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BASE COUNT ORIGIN

exon

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REFERENCE AUTHORS TITLE

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RESULT DCU93048

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338

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ACCESSION VERSION

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De, V.S., Schmidt, E.D., Van, H.G. and Hecht, V.F.
PRODUCTION OF APOMICTIC SEED
Patent: WO 9743427-A 20-NOV-1997;
                                  sequence.
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AC021198.2
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            thale cress.
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VRGTLCYIAPEYLSTGKSSEKTDVFGYGJMLLELITGQRAFDLARLANDDDVMLLDWV
KSLLKEKKLEMLVDDFDLENNYIDTEVEQLIQVALLCTQGSPMERFKMSEVVRMLEGDG
LAEKWDEWQKVEVIHQDVELAPHRTSEWILDSTDNLHAFELSGPR

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/db_xref="taxon:4039"
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/db_xref="GI:4756624"
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thaliana chromosome
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Submitted (00-FEB-2000) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
On Feb 11, 2000 this sequence version replaced g1:6693723.
On Feb 11, 2000 this sequence version replaced g1:6693723.
The sequence is of BAC F14D7 from Arabidopsis thaliana chromosome
1. The sequence does not represent the sequence of the entire
insert of this clone. It is shorter by 6954 bp because we submit
only the unique sequence of the clone. However, in order to
facilitate the joining of overlapping clones in the future for
creation of larger contigs, we provide small overlaps (200 bp)
between overlapping sumbitted clones. The 5' end of this sequence
overlaps by 200 bp to the 3' end of the sequence of the clone
F1504.
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                                                                                                                                                                                                                                                                                                                              CTATTCTTTATCTTTACGAGAACTATTTAACTGGTGTCATTCCCCCCGGAACTAGGCAACA 2645
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                                                                                                                                                     actcacggcaatcccaagcctttaaagttgttgacgtctcaagcaatgatttgtgtggga 682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (15-JAN-2000) P. Street, Albany, CA 94710, 3 (bases 1 to 81513)
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Structural Analysis of Arabidopsis thaliana Chromosome Unpublished (1998)
2 (bases 1 to 84440)
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Gene Structure 2; 1532-3, Yana, Kisaraz
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
Rosidae; Capparales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (20-APR-1998) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, Project
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Bevan, M., Brandt, P., I
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E-mail: michael.bevan@bbsrc.ac.
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NLELDSDSKAGLMQPARVSLMVDMLNDGSIETKINCARLIGRLVEEKGFRAELVSSHS
LLVGLKHLUKDDRRRNGVSPALJLLKSVSVHKQVRNLLVRIGAVPQLYDVLPCLDVEC
LESALFVLDSLCLESEGRIALKDSVNTIPHTVRLLMKVSEKCTNYAISILMSVCKLAS
ECSSLAVEVGLAAKLLLVIQSGCDPALKQRSELLKGLSHLTSDSNETSKYMAWLAR
SIANSKALEBDEDDDKHLNQQPSESVSBCQSSFGVKEDISSLTKTLRTQFWGVASFL
SQPSSSDDLQERNQTPDHPEEDEDLIAGIKNDFAEIGGRFRTGISKLSGNLFVSEFTK
LASNFLQLSSEDVDFKDYDYLGVTEELVAFVKDLAMHPETWLDFFLPDDDDSSDVKFK
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/translation="MGTYGSSQGQNGYLTSGSELARVAHGSRDELITGYSLKKSEKEK
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SVPRFQGGEALLMKKKDFVFKMPMFQPSKNGGFDGHILDLHSAVKDGYLGGGDGKFLV
VVTDEKKKLDLKEMISELELPEIPSVFTCPISLEPMQDPVTLCTGQTYERSNILKWFN
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SSEANTYLVEPLTVFPSFETAAVKLVNPVESSDVETDKHFLSKEIQIDEDKSVLEERS
TSTASSSRFINVQVDDEDDDDADDKLNDEETSSVSAIGGRSTTHHFFGEDEEDVSFSD
LEEEDDNEGGYKVSYKNLTNSGSDSSDKKSPDWVQLKEVKKSNDWLDVDAV
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4085. .4615,4671. .4960,5255. .5836)
/gene="F6H11.10"
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                                         1651.
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/chromosome="5"
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/variety="Columbia"
                1651. .1669
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                                                                          /gene="F6H11.10"
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DGDAKENNALIDEEPKKKKKKKKKKKRRGDTDDGEDEAVAEEEPKKKKKKKKKKKLQORGDT
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LSDNTYKSIKEMGFARMTQIQAKAIPPLMMGEDVLGAARTGSGCTLAFLIPAVELLYR
VKFTPRNGTGVLVICPTRELAIOSYGVAKELKKYHGQTVKVIGGEKKIETEAEILAKG
VNLLVATTGRLLDHLENTNGFIFKNLKFLVMDEADRILEQNFEEDLKKILNLLPKTRO
TSLFSATQSAKVEDLARVSLTSPYYLDVDEGREVTNEGLEGGYCVPSAMELLFLIF
FIKAEGKKKIMVFFSTCKSTKFHAELFRYIKFDCLEIRGGIDONKRTPTFLGFIKAE
TGILLCTNVAARGLDFPHVDMTYQYDPPDNFTDYIHRYGTTAGEGAKGKALLVLTFD
GELKFIQYLKAAKIPVEBHEFEEKKLLDYKFFYENLISENYALKESAKEAYKTYISGYD
BLKFIQYLKAAKIPVEBHEFEEKKLLDYKFFYENLISENYALKESAKEAYKTYISGYD
BLKFIQYLKAAKIPVEBHEFEEKKLLDYKFFYENLISENYALKESAKEAYKTYISGYD
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/note-"similarity to Myc-regulated DEAD box protein, Homo sapiens, PATCHX:S71758"
                              /number=6 complement(7445.
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complement(6581.
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GGKSKFERY"
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4961. .52
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/gene="F6H11.10"
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                                      gaagtetetggtetttttaeggettaatgaceaacegattgaeeggteeaateetagagea 623
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                                                                                                                                                                                                                                  CTTCTCCGGTCCATTAACTTGGGAGCTAGGAACGCTATCGAGTTTAAAATCAATGGATTT 84719
               GCCGGAGCTTGAAGTGTTACAGCTTTGGGAGAACAATTTCACCGGAAGCATCCCGCAGAA 84539
                                                                                                          cagcttggatctgtacaacaacaatcttacagggatagttcccactttcttgggaaaaatt 563
                                                                                                                                                             GTCTAACAACATGTTCACCGGAGAGATTCCAGCGAGTTTCGCAGAGTTGAAGAATCTCAC 84659
                                                                                                                                                                                                                                                                                                                           7.0%;
Similarity 52.3%;
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13830..13969,14562..14615))
/note="similarity to predicted protein, Arabidopsis thaliana, C80DDT21F"
/codon_start=1
/codon_start=1
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/number=3
complement(12363. .13829)
/number=3
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VVFHAVAGAKGSTAEQEYFIRKKNGGTLETEGQRERLRHCLVAAISRRASQGLKLEIR
TENKMGLLSDVTRVVRENGLSITRAEMCTQGEIAVGSFYVTDVNGGETGPSEVEAVVR
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rkaqvkdhldtvmeahhivgdvshvvvrvveakgvpvgmahterrlhelmygegdyen
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9707. .14616
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complement(10365. .10442)
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                                                                                                                                                                                                                                                                                                        Score 77.8; DB 7;
Pred. No. 1.2e-08;
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Convolvulaceae;
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Bassett,C.L., Cohen,R.A., Nickerson,M.L. and Rajeevan,M.S.
Direct Submission
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/ TLEARS LEALON-WAVAWIFLLSLCSTSSIYAAFALNSDGAALLSJTRHWTP IPSD
/ TLOSWNASDSTPCSWLGVBCDERGP VDTLNLSSYGISGEFGEDEISHLKHLKKVVLSGN
GFFGS IPSQLGNCSLLEHIDLSSNSFTGN IPDTLGALQNLRNLSLFFNSLIGPFPESSL
LSIPHLETYVFTGKCLNGSIPSNIGNNSELTTLWLDDWQFSGPVPSSIGNITTLQELY
LNDNNLVGTLPVTLNNLRNLVYLDVRNNSLVGAIPLDFVSCKQIDTISLSNNQFTGGL
PGLGNCTSLREFGAFSCALSGP IPSCFGQLTRLDTLYLAGRHFSGR IPPELGKCKSM
IDLGLQQNGLGEGEIFGELGMLSQLQYLHLYTNNLSGFVPLSIWKIGSLSLOLQNNL
SGELPVDMTELKQLVSLALYENHFTGVIPQDLGANSSLEVLDLTRNMFTGHIPDLCS
QKKLKRLLLGYNYLEGSVPSDLGGCSTLERLILEENNLRGGLPDFVEKQNLLFFDLSG
NRTTGFDFPSLGNLKANVTAIYLSSNQLSGSIPPELGSLVKLEHINLSHILKGLIPSE
LSNCHKLSELDASHNLLNGSIPSTLGSLTELTKLSGENSFSGNSDLCINCPADGLACPES
SILRPCNMGSNTGKGGLSTIGIAMIVLGALLFIICLFFSGNSDLCINCPADGLACPES
SILRPCNMGSNTGKGGLSTIGIAMIVLGKALFFIICLFFSAFFLHCKKSVDEIAISA
QEGDGSLLAKVLBALTSLNLSNCTGGKAAGTITKATLSPAFFLHCKKSVDEIAISA
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45 Wiltshire Road, Kearneysville, WV 25430, USA
Location/Qualifiers
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                                                                              SMVREIETIGKVRHRNLIKLEEFWLRKEYGLILYTYMENGSLHDILHETNPPKPLDWS
TRHNIAVGTAHGLAYLHFDCDPAIVHRDIKPMNILLDSDLEPHISDFGIAKLLDQSAT
SIPSNTVQGTIGYMAPENAFTTVKSRESDVYSYGVVLLELITRKKALDPSFNGETDIV
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/gene="inrpk1"
                                       GWYRSYWTQTGEIQKIYDPSLLDELIDSSYMEQYTEALSLALRCAEKEYDKRPTMRDV
YKQLTRWSIRSYSSSYRNKSK"
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/protein_id="AAB36558.1"
/db_xref="GI:1684913"
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1641 AGAAACTGTTTATTTCACTGGCAATGGTCTTAATGGTTCAATCCCCTTCAAA 1691
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Local Similarity 49.1%;
hes 202; Conservative
                                                                                      Direct Submission

AL Submitted (30-Nov-1999) to the DDBJ/EMBL/GenBank databases. Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program, Kannondal 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp,
URL:http://www.dna.affrc.go.jp,
URL:http://www.dna.affrc.go.jp.82/, Tel:81-298-38-7441,
Fax:81-298-38-7468)
The orientation of the sequence is from T7 to SP6 of the PAC clone. Genes were predicted from the integrated results of the following:GENSCAN1.0, BLASTN2.0, BLASTN2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against the non-redundant database NRP (PIR, SWISSPROT, GENPEPT, PDB) from MAFF DNA bank and the cDNA sequence database at RGP. Protein similarities of the cording regions were searched against NRP with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RCP clone TD.
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Sasaki.T., Matsumoto.T. and Yamamoto.K.
Oryza sativa nipponbare(GA3) genomic DNA,
clone:P0003H10
Detailed information on assemble quality together with annotation of this entry at http://www.dna.affrc.go.jp:82/genomicdata/Genomer
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FEATURES
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/note-"ESTS D47452(S12946),C23573(S10086),C19173(E10057),  
AU081294(E10057),AU032455(S10086) correspond to a region  
AU081294(E10057),Similar to PNIL34. (U37437)
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phpringiirecggkninaeromadaardefealeknydeagnerriochteliksukrindeferiksiksalyreks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_1d="baa87823.1"
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PVVAEIFSLMSRDEARHAGFLNKGLSDFNLALDIGFLTKARKYTFFKPKFIFYATYLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAHKDGNDGSLLKSMAGEPLSVVLIVYTFVSVWFVGGLIVFHLYLMSTNQTTYENFRY
RYDKKENPYNRGAISNIAEVFCAGIPPSMYNFRSWVAPPPLEEPDDVSGQLPPRNGAD
LTGGVKEKVDLEMGRNGGIIPAILRGLDYDEMEKNDVSVHIKDRGAAPAAPDPFWAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MGEPNQRRLYQVWQGSNKFLCGGRLIFGFDAGSLFLSTYLIVAP
LVGLCCQCITKNNSISSEKQYLGLFVLLATIVLGHADLAFLLMTGSRDPGIVFRNARF
PESCGGGDEBECVAGDVTTPSAEWTAASPHLALLFRSKDVVVNGCVYKVKCDTCLLXF
PPRASHCSICNNCVRKFDHHCPWVGQCIGLRNYRFFFLFISTSTLLCVYVFVVSWLNI
                                                                                                                                                                                 join(22475. .22550,23332. .23705)
/note="ESTS AUG30013(E50493), 2010 of the predicted gene.; Similar to O.sativa
to a region of the predicted gene; Similar to O.sativa
gene encoding calmodulin. (Z12828)"
                                                                                                                                                                                                                                                                                                                                                                       NY IEDLLKNIRTQVLLKLIKPYTRIRIPFISQKWCMKIISNMELWY ILVLFHGTLYYT RAILGSCKKYSLKLDLFLSCAQTRVQLKSCALNRADPMLFLTEVNLLSYSVQDALSSI VLSMFCMELNFPEKDVELLYSLLDNRIQGHIDQVNKLLERGDREIFPEHRQVEYSAE EHLPNGVQQSMYREIAGCLGCTALGTCLHVLLMWMLGFCPELNLSANSNESETILASM ARNFWFCWHCRTSKFWYGRENVWFRVKYAPGTRHTANIVPLPSSDSVANQSLSNQNEG KESPFLSYTTDQQALNLQREHTTLSDNVINLSEGSYRPLAPSSHLGHFVYTIFYVDDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    //note="ESTS AU081256(C53656), AU081257(C53656),
AU03236(R3784), AU081351(E61905), AU031587(E61905),
AU081361(R3784) correspond to a region of the predicted
gene.; Similar to alien-like protein. (AC005623)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(13373 . 13457,15836 . 15914,17237 . 17477,17560 . 1
17726 . 17860,18400 . 18587,18681 . 18749,18826 . 18916,
19028 . 19162,19323 . 19379,19349 . 19441,19450 . 19509,
19523 . 19585,19589 . 19701,19800 . 19941,20057 . 20294,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVENPEFKRKLDRMVEINKKIIAIGESDDIPLVKNLKRIPHVAALVSEIIAAYLMPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKIGYWRYITIFRHLKANPEYQVYPIFKYFENWCQDENRHGDFFSALLKAQPQFLNDW
KAKLWSRFFCLSVYVIMYLNDCQRTTFYEGIGLDTKEFDMHVIIETNRTTARIFPAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WHNEDCESTPTAVSHHVNSERL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Statiar to Arabidopsis thaliana DNA chromosome
BAC clone F22K18 (AL035356)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4530"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESGSVDFAEFEPQLVY"
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/protein_id="baa87825.1"
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/tignslation="maddlfiddojiaefkeafslfdkdgdggittkelgtymrslgonp
TeaelQdminevdadgngtidffeflnlmarkmkdtdseeelkeafrvfdkdqngfis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Oryza sativa"
                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21586)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2951,3129. .3317,3521. .3850,4405. .4638,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .17634,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
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TRGHALAEPEPHASPRLVGHRGSRRRSPSPPSPPLPVTARCEEEHRRRHRCSSLPPR
ROMRRGAPPDPASPCEDLATIGVGRRWKKWDAEEGVGVAEEEEMAARGRARQLRGG
GGGVVVAHKRRSGAREERRCGGFERRSGGDERGKEEPVGRRENKGERIGE
TDERRWFGHSHKPSIILMWIQTTKPARRRGANVLARHGGDDRRRRCRSQCAVARRQE
ALPIGSLFPYLJFMIRDLKVAKBEQDIGFYAGFVASCIVQAYASEVCRKEHQALGISL
VTSSRAIALVVGPAIGGFLSQETLHMHHDDKEVIDALEAQDATSDLGETTKESGSGRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAELRHYMTNIGEKLIDEEVEEMIREADVDGDGQINVDEFVKVMMAK"
complement(join(24778 . .24897,25615 . .25722,58008 . .25893
26090 . .26177,26435 . .26583,27519 . .27881,27708 . .27778,
28329 . .28389,28512 . .28552,29058 . .29225,30476 . .31136))
//note-"hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAA87827.1"
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join(40347..40358,40468..40680)
/note="hypothetical protein"
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53657. .53800,54663. .54734,56026. .56334))
/note="ESTS C97644(C60871),AU081265(C60871)
a region of the predicted gene.; Similar to
LRP gene. (X95269)"
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IQSSFEWGYLLTQIAGGIWADTVGGKTVTLGFGVTWMSIAFALTPFAXKLEPFLLTHNFGW
AFMGVGEGVAMPAMNNILSKWVPVSERSRSLALVYSGMYLGSVTGLAFSPLLIHNFGW
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50202. .50411,50488. .50625,50842. .50943,51105. .51170,
51274. .51358,51454. .51551)
/note="Similar to Arabidopsis thaliana chromosome II BAC
727A16 sequence; hypothetical protein. (AC005496)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MHPKNHLVAAATVILVLQSPLPSSSFSNRRRRRQCRPTIALAT
ADGSTREVLPPPDRGGGGGFRRWHMKEGGD"
complement(join(42025. .42083,43481. .43661))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASLLKNMFANKKEMTNQSISLLDAGFHGRKSTLLGCSYQVKQQGSSKP" complement(join(34468. .34544,37202. .37385))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GHTKSLLKNWQLMSAITLYCVFSLHDTAYLEIFSLWAVSSRKYRGLSFTSQDVGIVLA
ISGFGVLVYQLAIYPLLAKYVGPIKPFRYAAVLSILLLSTYPFMANLYGLELKVLINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAA87826.1"
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EGGWIADTLVSRGLSVTTVRKIMQSIGELGPAFELTQLSHIDSPAMAVLCMACSQGTD
AESQSGLYSNHQDIGERYAGVLLGLSNTAGVLAGVEGTAATGYILQHGSWDDVEKVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation-"MAAGDKAGGDDAAAAAPLLVPAAAAGRRRRCPGCRTKERCEAHPG
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join(47081. .47084,47194. .47313,47469. .47584)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAA87828.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MWFQTSTSDARTHGSGDRGSAGRIRACRGTTRSAAPGLGSREAT/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                          VLYLVGTLVWNLFSTGEKIID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSVFYSFGSLGVFWFSTWASKAYSSPLEDPGISAEEKKLITSQTTGGEPVKEIPWGLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=
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/db_xref="GI:6498429"
                                                                     /codon_start*:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="hypothetical protein"
                                                                                                                                                                                                                                                             .53299,53395. .53466
                                                                                                                                               correspond to
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translation="MAAAWSPALAAVLLAAAVASASNSEGDALYALRRALADPRGVLQ"

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Search completed: June 24, 2000, 00:15:32 Job time: 45887 sec
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.9%; Score 75.8; DB 7; Length 1.
Best Local Similarity 67.3%; Pred. No. 3.6e-08;
Matches 107; Conservative 0; Mismatches 52; Indels
                                                                                                                                                                                                         53685 CTTGGCAAGCTGAGTTCCTTAGTATTCTTGTGAGTAACT 53647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
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                                                                                                                                           SWDPTLYNPCTWFHYTCDRAGRYTRLDLGNSNLSGHLAPELGHLEHLQYLELYKNNIQ
GTIPAELGSLKNIISLDLYNNNITGTIPKELGKLSSLYFLRLMDNSLMGPIPRDLAKI
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59608. 59826
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EGSTSDEWEGRGGEGRGGAANVEPAGEERRRHAETKLGLSILVGGRGAPHRQSGGHG
EGGRDEEGELMLVGGALRPEEEEEEGHGRRRGEERRRVCEREREER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 142418;
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Tomato Cf-9 cDNA.
Tomato pathogen re
Tomato Cf-9 gene.
Tomato pathogen re
Human nuclear prol

Dictyostelium plas Plasmodium var-7 g Sequence encoding

Tomato pathogen re Clone hTS16 encodi Sequence of varian

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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D 20-NOV-1997.
D 20-NOV-1997.
EG2443.
F 13-MAY-1996; GE-010044.
R 14-MAY-1996; GE-010044.
A (NOVS) NOVARTIS AG.
D VOTARTIS SC. Hecht VFG, Schmidt EDL, Van Holst GJ;
R WPI; 98-086529/08.
R P-PSDB; W47018.
T Production of apomictic seeds - useful in plant breeding
S Claim 28; Pages 71-73; 123pp; English.
T Production of apomictic seeds - useful in plant breeding
S Claim 28; Pages 71-73; 123pp; English.
C SERK LERR (leucine-rich repeat) sequences.
C SERK LERR (leucine-rich repeat) sequences.
C Sequence 1106 BP; 331 A; 258 C; 206 G; 311 T;
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Best Local Similarity 100.0%;
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cgtgtggatttgggaaattcaaacctctctggacatcttgcgcctgagcttgggaagctt
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/note= "shows high homology to SERK"
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Score

Query Match

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Minimum Maximum

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Total number

Post-processing:

Database

Title: Perfect score:

Scoring table: Sequence: 8

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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v06587;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST cl
receptor kinase; apomixis; apomictic; seeds; pr
plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
Arabidopsis thaliana.
Arabidopsis thaliana.
Arabidopsis thaliana.
Arabidopsis thaliana.
104..760
W09743427-A1.
20-N0V-1997, E02443,
13-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, 98-08529/08.
P-PSDB; W47019.
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The sequence is that of an EST clone showing SERK LRR (Leucine-rich repeat) sequences.
Sequence 981 BP; 286 A; 236 C; 180
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Local Similarity 98.
hes 952; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           ACCTTCCGAACTTGGAAATCTGAAGAATCTCATCAGCTTGGATCTGTACAACAACAATCT
  aagtatatatatgtagtaaaaacaacaaaaaatgaagcaatcgaatcggtaatatcatctgg
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851 688 791 731

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709

__ed. No. 1.3e-225;
Mismatches 10 plant high <u>ი</u> breeding Indels 279 H ç 2: Gaps 72 2

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20-NOV-1997
13-MAY-1997; E02443
14-MAY-1996; GB-010044
14-WAY-1996; GB-010044
(NOVS) NOVARTIS AG
(NOVS) NOVARTIS AG
PPSDB; W47022.
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Arabidopsis thaliana SERK LRR homologous EST receptor kinase; apomixis; apomictic; seeds; plant breeding; leucine-rich repeat; ss. Arabidopsis thaliana.

Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Production of apomictic seeds - useful in plant br Claim 28; Pages 86-88; 123pp; English. The sequence is that of an EST clone showing high SERK LRR (leucine-rich repeat) sequences. Sequence 1063 BP; 313 A; 242 C; 206 G;
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                                                ccaaggaactataccttccgaacttggaaatctgaagaatctcatcagcttggatctgta
                                                                                                                   agcaaactccgaaggagatgctctctacgctcttcgccggagtttgacagatccagacca
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caacaacaatcttacagggatagttcccactttcttgggaaaattgaagtctctggtctt
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1.2e-222;
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RESULT
V06588
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Query Match
Best Local Similarity 96.
Matches 753; Conservative
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20-N0V-1997; E02443.
13-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, $
WPI; 98-086529/08.
                                                                                                                                                                                                                                                              03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous receptor kinase; apomixtis; see plant breeding; leucine-rich repeat; ss. Arabidopsis thaliana.
Arabidopsis thaliana.
Key
2. .664
                                                                                                                                                                                                                                                                                                                                                       V06588;
                                                             Production of apomictic seeds - useful in plant by Claim 28; Pages 79-80; 123pp; English.
The sequence is that of an EST clones showing high SERK LRR (leucine-rich repeat) sequences.
Sequence 788 BP; 234 A; 191 C; 156 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                     1020
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Score 714.2; DB 1;
Pred. No. 2.2e-172;
0; Mismatches 28;
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V06589;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST cl
receptor kinase; apomixis; apomictic; seeds; pr
plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
Location/Qualifiers
CDS
1..678
W09743427-A1.
20-N07-1997.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
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RESULT V06591 ID VC AC VC DT 03 DE AI

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Best Local Similarity 71.9%;
Matches 532; Conservative
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P-PSDB; WA7021.

Production of apomictic seeds - useful in plant br Claim 28; Pages 83-84; 123pp; English. The sequence is that of an EST clones showing high SERK LRR (Leucine-rich repeat) sequences.

Sequence 894 BP; 270 A; 163 C; 176 G;
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GTACCAAGTGTTTGTAAATC
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                            CTTAAAAAGAAGTTGAAGAACCTATAAAGAAGAA-TGTTAGGTGACCTTGTAAGAACTCT
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Pred. No. 7.5e
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Claim 27; Pages 91-95; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase.

CI thay be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant preeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the propagated hybrids and could shorten and simplify the breeding programs that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with Specific stable traits for such characteristics as height, seed and forage quality and maturity.

Squence 2089 BP; 568 A; 419 C; 503 G; 599 T;
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 314
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20-NOV-1997.
13-MAY-1997; E
14-MAY-1996; C
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                                                                                                                                                                                                                                                              aaccaagacaaccgcgtcactcgtgtggatttgggaaattcaaaacctctctggacatctt
                                                                                                                                                                                                                                                                                                                                                                   gcaaactccgaaggagatgctctctacgctcttcgccggagtttgacagatccagaccat
gcctttaaagttgttgacgtctcaagcaatgatttgtgtgggacaatccccaacaacgga
                                                                                                                                                         caaggaactataccttccgaacttggaaatctgaagaatctcatcagcttggatctgtac
                                                                                                                                                                                          GTTCCAGAGCTTGGTGTGCTCAAGAATTTGCAGTATTTGGAGCTTTACAGTAACAACATA
                                                                                                                                                                                                            gcgcctgagcttgggaagcttgaacatttacagtatctagagctctacaaaaaccaacatc
                                                                                                                                                                                                                                                                                                              GCTAATTTGGAAGGTGATGCTTTGCATACTTTGAGGGGTTACTCTAGTTGATCCAAACAAT 329
                                   CTCCGGCTTAACAACAGTCTCACTGGGTCAATTCCTATGTCACTGACCAATATTACT
                                                                                                              aacaacaatcttacagggatagttcccactttcttgggaaaattgaagtctctggtcttt
                                                                                                                                          ACTGGCCCGATTCCTAGTAATCTTGGAAATCTGACAAACTTAGTGAGTTTGGATCTTTAC
                                                                                                                                                                                                                                                                                                GTCTTGCAGAGCTGGGATCCTACGCTAGTGAATCCTTGCACATGGTTCCATGTCACTTGC
                                                            ttacggcttaatgacaaccgattgaccggtccaatcctagagcactcacggcaatcccaa
                                                                                        TTAAACAGCTTCTCCGGTCCTATTCCGGAATCATTGGGAAAGCTTTCAAAGCTGAGATTT
                                                                                                                                                                                                                                               AACAACGAGAACAGTGTCATAAGAGTTGATTTTGGGGGAATGCAGAGTTATCTGGCCATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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195. .2072
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/product= SERK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apomixis;
                                                                                                                                                                                                                                                                                                                                                                                                                  17.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 191; DB 1;
Pred. No. 1.9e-39;
0; Mismatches 205
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                                                                                                                                                                                                                                                                                                                                                                                                       205;
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V06571
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Best Local s
Matches 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant the redding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed apomictic plant. Apomixis provides for true-breeding, seed propagated hybrids and could shorten and simplify the breeding process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.

Seguence 1814 BP; 530 A; 354 C; 415 G; 515 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 21; Pages 47-51; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plant breeding; ss.
Daucus carota.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       De Vries SC, Hecht
WPI; 98-086529/08.
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De Vries SC, Hecht VFG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9743427-A1.
20-NOV-1997.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Daucus carota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                  399
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  639
                                                318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCCTTCAAGTGTTAGATCTATCAAATAACAGACTCTCTGGTTCAGTTCCTGACAATGGC
                                                                                                                                                                                                                                                                                                                                                                tgcgcctgagcttgggaagcttgaacafttacagtafctagagcfcfacaaaaaacaacaf 458
                                                                                                                                                                                                                                                                ccaaggaactataccttccgaacttggaaatctgaagaatctcatcagcttggatctgta 518
                                                                                                                                                                                                                                                                                                                                  TGATGCTTACCTTGACAAATATGGGGGTTCTTATGACATTGGAGCTTTACAGCAATAACAT 197
agcctttaaagttgttgacgtctcaagcaatgatttgtgtgggacaatcccaacaaacgg
                                                CTTGCGTCTCAACAACAACAGCCTCTCTGGTCCAATTCCAATGTCACTGACTAATATTAC
                                                                            tttacggcttaatgacaccgattgaccggtccaatcctagagcactcacggcaatccca
                                                                                                                                           CATGAATAGCTTCTCTGGACCTATACCGGACACATTAGGAAAGCTTACAAGGCTAAGATT
                                                                                                                                                                                                                                      AAGTGGACCAATTCCTAGTGATCTTGGGAATCTGACAAATTTGGTGAGCTTGGACCTATA
                                                                                                                                                                                      caacaacaatcttacagggatagttcccactttcttgggaaaattgaagtctctggtctt
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                                                                                                                                                                                                                                                                                                                                                                                                                             h 7.6%;
Similarity 52.1%;
88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 94. .1755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA;
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Pred. No. 2.3e
0; Mismatches
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nes 173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1814;
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Daucus carota SERK gene.
receptor kinase; apomixis
plant breeding; ds.
Daucus carota.
Key
                                                                                                                                                20-NOV-1997.
13-MAY-1997; ED2443.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, SWPI; 98-086529/08.
        production of apomictic seeds - useful in plant breeding Claim 21; Pages 40-46; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides
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V06570;
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  advantages
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5295. .58
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6197. .63
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/*tag= g
/number= 6
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  improvement
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   and
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   cultivar
  development
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Best Local
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20-NOY-1997;
20-NOY-1997;
13-MAY-1997; E02443;
14-MAY-1996; GB-010044.
(NOYS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed propagated hybrids and could shorten and simplify the breeding process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.

Sequence 6695 BP; 1844 A; 1182 C; 1243 G; 2422 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
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Arabidopsis thaliana SERK
receptor kinase; apomixis;
plant breeding; ds.
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Pred. No. 1.4e
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The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac: The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with seed apomixis allows plant breeders to develop cultivars with seed and forage quality and maturity.

Sequence 4081 BP; 1120 A; 770 C; 785 G; 1406 T;
p-PSDB; wi3408.

DNA encoding plant morphogenesis regulatory protein - useful plants with short stems or altered inflorescence yield plants with short stems or altered inflorescence claim 1; Pages 6-10; 17pp; Japanese.

The present sequence encodes an Arabidopsis thaliana plant morphogenesis regulatory protein (MRP), which can be used to a plant with, e.g. short stems or altered inflorescence. The acts on a plant at a specific site for a specific period, and
                                                                                                                                                                                                                                        04-MAR-1997.
24-AUG-1995; JF-216187.
24-AUG-1995; JF-216187.
24-AUG-1995; JF-216187.
(MITS-) MITSUI GYOSAI SHOKUBUTSU
(CHIK-) ZH CHIKYU KANKYO SANGYO (
WPI; 97-206629/19.
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P-PSDB; W47017.
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Arabidopsis thaliana plant morphogenesis regulatory protein cDNA.
Plant; morphogenesis; regulation; short; stem; alteration;
inflorescence; extraneous; gene; expression; transformation;
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/note- "plant morphogenesis regulatory protein"
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Best Local
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11-MAY-1995; G01075.
11-MAY-1994; GB-009394.
23-DEC-1994; WO-G02812.
31-MAR-1995; GB-00658.
07-APR-1995; GB-007232.
                           Increasing plant pathogen resistance by induction of variegation—may lead to acquired resistance to a broad range of pathogens.

Claim 9; Page 85-87; 31pp; English.

T06307 is a tomato pathogen resistance gene Cf-2.2 partial cDNA clone. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagales of plants) containing such constructs. Cf-2.2 imparts resistance to the disease caused by the leaf mould fungal pathogen Cladosporium fulvum. C.fulvum contains avirulence (Avr) genes that confer recognition by plants containing Cf-genes, leading to the activation of host defence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therefore be used to regulate extraneous gene expression plant. The MRP'S CDNA or genomic DNA can be used to transplant to increase its MRP expression, and therefore control (particularly stem length) of the plant.

Sequence 3176 BP; 927 A; 654 C; 659 G; 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1406
                                                                                                                                                                                                                       (GATS-) GATSBY CHA)
Hammond-Kosack KE,
WPI; 96-010949/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1466
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                                                                                                                                                                                                                                                                                                                                                                     Lycopersicon W09531564-A2.
                                                                                                                                                                                                                                                                                                                                                                                                   Partial tomato pathogen resistance gene Cf-2.2 Pathogen resisitant; Cf-2.2; tomato; C.fulvum; leaf mould; variegation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1526 AGAAGA 1531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1286 CAACAATATCAAAGGTCCAATCCCGGTTGAGCTATCTCGTATCGGTAACTTAGATACATT 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1226 TGGCACTATACCCCGAGCATTTCAAAAGCTAGAAAGTATGACTTACCTTAATCTGTCCAG
plants containing Cf-genes, leading mechanisms to attack the disease. Sequence 3573 BP; 1032 A; 6:
                                                                                                                                                                                                            P-PSDB; R85299
                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-APR-1996 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106307 standard; cDNA; 3573
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KE, Jones
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Pred. No. 7.1e-09;
0; Mismatches 147
                                                                                                                                                                                                                                          Jones JDG;
 654
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Avr 4; Avr 9;
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Query Match Best Local Similarity

52.2%;

Score Pred.

No.

DB 1; 3.9e-07;

Indels

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Query Match
Best Local Similarity
Matches 142; Conser
                                                                                                                                                                                                                                                                             23-NOV-1995.
11-MAY-1995; G01075.
11-MAY-1994; GB-009394.
23-DEC-1994; WO-G02812.
31-MAR-1995; GB-006658.
07-APR-1995; GB-007232.
                                                         increasing plant pathogen resistance by induction of variegation may lead to acquired resistance to a broad range of pathogens.

Claim 9; Page 80-83; 131pp; English.

T06306 is the tomato pathogen resistitance gene Cf-2.1. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagules of plants) containing such constructs. Cf-2.1 imparts resistance to the disease caused by the leaf mould fungal pathogen Cladosporium fulvum.

C.fulvum containing Cf-genes, leading to the activation of host defence mechanisms to attack the disease.

Sequence 6471 BP; 2073 A; 1106 C; 1122 G; 2170 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1235
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                                                                                                                                                                                                                               (GATS-) GATSBY CHARITABLE Hammond-Kosack KE, Jones WPI; 96-010949/01. P-PSDB; R85298.
                                                                                                                                                                                                                                                                                                                                                                                                           mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                  signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142;
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  Conservative
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5015. **
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1745
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= immature_Cf-2.1_protein
1677. .1745
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1. .1676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA; 6471
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          52.2%;
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                                                                                                                                                                                                                                                       DA, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene Cf-2.1.
1: tomato; C.
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Score 64; DB 1;
Pred. No. 4.8e-07;
0; Mismatches 130
                                                                                                                                                                                                                                                         Jones JDG;
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                         Length 6471;
  Indels
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TTACTGAACTATTTTTGGGTAATAACTCTCTTAATGGCTCTATTCCTGCTTCATTGGGGA 2082

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RESULT
V14518
                                                                                                                                                                                  PS Claim 3; Fig 1a; 75pp; English.

PS Claim 3; Fig 1a; 75pp; English.

CC This sequence is an example of the polynucleotide of the invention, and CC is able to confer pathogen resistance on a plant. It is one of two tomato CC is gene variants, which offer resistance against the pathogen CC CF-5 gene variants, which offer resistance against the pathogen CC cladosporium fulvum-5. Transgenic plants can be produced by incorporating CC the gene into plant cells and regenerating plants from the cells; CC assaually produced offspring can also be subsequently CC produced. Expression of the gene in plant cells can confer pathogen CC resistance on a plant e.g. to tomato leaf mould (C. fulvum) in tomatoes. CC oligonucleotides with sequences complementary to the gene expression. The CC identify other genes/fragments conferring pathogen resistance on plants CC identify other genes/fragments conferring pathogen resistance on plants CC e.g. phytophthora resistance in potatoes. Homologies between Cf-5 and CC cf-9 may be used to identify further resistance genes of this class.

SQ Sequence 3979 BP; 1217 A; 717 C; 698 G; 1347 T;
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20-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tomato gene Cf-5, confers resistance to Cladosporium fulvum -
for production of transgenic plants resistant to pathogens e.c
tomato leaf mould C. fulvum in tomatoes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dixon MS, Hatzixanthis K, WPI; 98-008895/01.
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20-NOV-1997.
08-MAY-1997; G01249.
24-SEP-1996; GB-019924.
09-MAY-1996; GB-009681.
(INNE-) INNES CENT INNOVATIONS LTD JOHN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CF-5 pathogen resistance gene variant #1.
Tomato; CF-5 pathogen resistance gene; Cladosporium fulvum-5; tomato leaf mould; Phytophthora resistance; ss.
Lycopersicon pimpinellifolium.
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tcactcgtgtggatttgggaaattcaaacctctctggacatcttgcgcctgagcttggga 415
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                                                                                      Similarity
                                                               Conservative
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/product=
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653. .3560
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                                                                                   48.8%;
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                                                         Score 61.2; DB 1;
Pred. No. 2.1e-06;
0; Mismatches 173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is an example of the polynucleotide of the invention, and clist able to confer pathogen resistance on a plant. It is one of two tomato CC F-5 gene variants, which offer resistance against the pathogen cC Cladosporium fulvum-5. Transgenic plants can be produced by incorporating the gene into plant cells and regenerating plants from the cells; cC asexually or sexually produced offspring can also be subsequently cC produced. Expression of the gene in plant cells can confer pathogen cC resistance on a plant e.g. to tomato leaf mould (C. fulvum) in tomatoes. CO iligonucleotides with sequences complementary to the gene or fragments cC of it, are useful in anti-sense techniques to reduce gene expression. The nucleic acids/polynucleotides are useful as hybridisation probes to identify other genes/fragments conferring pathogen resistance on plants cC e.g. Phytophthora resistance in potatoes. Homologies between Cf-5 and CC cf-9 may be used to identify further resistance genes of this class.

So Sequence 3979 BP; 1218 A; 716 C; 698 G; 1347 T;
                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 165
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20-NOV-1997; G01249.
24-SEP-1996; GB-019924.
29-MAY-1996; GB-009681.
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(INNE-) TO MATERIAL TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME TO ME
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Tomato; CF-5 pathogen resistance gene; Cladosporium tomato leaf mould; Phytophthora resistance; ss.
Lycopersicon pimpinellifolium.
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356 tcactcgtgtggatttgggaaattcaaacctctctggacatcttgcgcctgagcttggga 415

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                                                                             Pr Tomato gene Cf-5, confers resistance to Cladosporium fulvum - useful pr for production of transgenic plants resistant to pathogens e.g. Pr tomato leaf mould C. fulvum in tomatoes

PS Disclosure; Fig 7; 75pp; English.

CC This sequence is a clone of the polynucleotide of the invention, which offer creates a clone of two tomatoes of a plant. The polynucleotide of the invention is one of two tomato CF-5 gene variants, which offer creatistance against the pathogen resistance on a plant cells and cc resistance against the pathogen Cladosporium fulvum-5. Transgenic plants can be produced by incorporating the gene into plant cells and cc regenerating plants from the cells; asexually or sexually produced confepring can also be subsequently produced. Expression of the gene in confer pathogen resistance on a plant e.g. to tomato leaf complementary to the gene or fragments of it, are useful in anti-sense techniques to reduce gene expression. The nucleic acids/polynucleotides care useful as hybridisation probes to identify other genes/fragments conferring pathogen resistance on plants e.g. Phytophthora resistance in potatoes. Homologies between Cf-5 and Cf-9 may be used to identify sequence 4123 BP; 1253 A; 742 C; 725 G; 1403 T;
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   Query Match
Best Local Sin
Matches 165;
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V14523;
20-MAY-1998
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20-NOV-1997.
08-MAY-1997; (
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Tomato: CF-5 pathogen resistance gene; Cladosporium
tomato leaf mould; Phytophthora resistance; ss.
Lycopersicon pimpinellifolium.
Key
Location/Qualifiers
CDS
603. .3002
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24-SEP-1996; GE-019924.
29-MAY-1996; GE-009681.
(INNE-) INNES CENT INNOVATIONS LTD JOHN.
The Hatzixanthis K, Jones DA, Jones
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                    Similarity
   Conservative
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                  48.8%;
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 Score 61.2; D
Pred. No. 2.1e
0; Mismatches
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                  DB 1;
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Search completed: June 23, 2000, 22:52:36 Job time: 40552 sec

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Title:
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No.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
39
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37.8
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48.6
49.6
60.8
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1: /cgn2_6/ptodata/;

2: /cgn2_6/ptodata/;

3: /cgn2_6/ptodata/;

4: /cgn2_6/ptodata/;

5: /cgn2_6/ptodata/;

6: /cgn2_6/ptodata/;

7: /cgn2_6/ptodata/;
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Match Length
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1106
GenCore version 4.5
Copyright (c) 1993 - 2000 Com
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US-08-913-257-1
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US-08-475-891A-1
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us-08-508-786-2	US-08-846-338-13	US-08-401-068-13	US-08-909-965C-16	US-08-623-906A-16	US-08-478-675-99	US-08-120-827-99	US-07-867-106-2	US-08-724-394A-22	US-08-724-394A-21	US-08-724-394A-20	US-08-859-201-1	US-08-602-264A-1	US-08-618-911-5	US-08-618-911-3	US-08-883-515-1	US-08-252-626A-1	บร-08-189-256A-11
Sequence 2, Appli	Sequence 13, Appl	Sequence 13, Appl	Sequence 16, Appl	Sequence 16, Appl	Sequence 99, Appl	Sequence 99, Appl	Sequence 2, Appli	Sequence 22, Appl	Sequence 21, Appl	Sequence 20, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 5, Appli	Sequence 3, Appli	GENERAL INFORMAT	Sequence 1, Appli	Sequence 11, Appl

ALIGNMENTS

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REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0237
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
TITLE OF INVENTION: Disease Resistance in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FIRM: PC DOS/MS-DOS
OPERATING SYSTEM: PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION UNBER: US/08/475,891A FILING DATE: 06-JUN-1995 CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/373,375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
                                                                                                                                               MOLECULE TYPE:
         OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Two Embarcac
CITY: San Francisco
                                                                               NAME/KEY: CDS
LOCATION: joi
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join(1648..4383, 5178..5513)
WATION: /product= "RRK-F"
WATION: /note= "Xa21 Xanthomonas spp. disease
RWATION: resistance gene RRK-F from rice (Oryza
                                                                                                                                                                             linear
                                                                                                                                               DNA (genomic)
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; OTHER INFORMATION: Sativa) TUS-08-475-891A-1
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US-08-567-375-1
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Best Local Similarity 50.8
Matches 167; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3035 GCACCAACAATTCAGTGGTTGGATACCA 3063
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                                                                                                             APPLICATION NUMBER: US 60
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 07-JUN-1995
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                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                        APPLICATION NUMBER: US/08/567,375
FILING DATE: 04-DEC-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        542 ttcccactttcttgggaaaattgaagtctctggtctttttacggcttaatgacaaccgat 601
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                                                                                               PRIOR APPLICATION DATA:
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                                                         APPLICATION NUMBER: US 08/373,375 FILING DATE: 17-JAN-1995
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Song, Wen-Yuang
Kevin L.

MBER: 34,774
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                                                                                                                                                                                          US 60/004,645
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                                                                                                                                     US 08/475,891
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OTHER INFORMATION:
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US-08-567-375-1
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GENERAL INFORMATION:
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO: 1:
COUNTR: COUNTRE PAINT AND COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
COMPUTER: FROM PC COMPATIBLE PC-DOS/MS-DOS
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LENGTH: 6256 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
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                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                        SSEE: Townsend and Townsend and Crew LLF
T: Two Embarcadero Center, Eighth Floor
San Francisco
                                                                                                                                         California
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RAMATION: /product= "RRK-F"
RRATION: /note= "X821 Xanthomonas spp.
RMATION: resistance gene RRK-F from ric
RMATION: (Oryza sativa)"
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Pred. No. 7.6e-07;
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Patent No. 5952485

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; LOCATION: join(1648; OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORM
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Matches 167; Conservi
Sequence 3, Application US/08567375
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
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PRIOR APPLICATION NUMBER: US 00
APPLICATION NUMBER: US 00
FILTING DATE: 17-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
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APPLICATION NUMBER: US/0
FILING DATE: 17-JAN-1996
CLASSIFICATION: 800
                                                                                                                                                                             3035 GCACCAACAAATTCAGTGGTTGGATACCA
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TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 34,774
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RMATION: /product= "RRK-F"

RMATION: /pote- "Xa21 Xanthomonas spp. disease

RMATION: resistance gene RRK-F from rice (Oryza

RMATION: sativa)"
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Pred. No. 7.6e-07;
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                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 163; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 08/
FILING DATE: 17-DAN-1995
ATTORNEY/AGENT INFORMATION:
ANASC. ESCALISION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UNBER: US/08/567,375 FILING DATE: 04-DEC-1995 CLASSIFICATION: 800 PRIOR APPLICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/004,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
                                                               1279 GGCATTCTACTCGCCTACGAAAACAACTTGAGCGGTTCGATCCCGTTGGCCATAGGAAAT 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                             1159 AAGATCACAGGAAGCATTCCGAAGGATATTGGCAATCTTATTGGCTTACAACATCTCTAT 1218
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                                                                                                                                                                                442 ctctacaaaacaaccatccaaggaactataccttccgaacttggaaatctgaagaatctc 501
                                                                                                                                                                                                                                                                    382 aacctctctggacatcttgcgcctgagcttgggaagcttgaacatttacagtatctagag 441
562 ttgaagtototggtotttttacggottaatgacaacogattgacoggtocaatcotagag 621
                                                                                         502 atcagcttggatctgtacaacaatcttacagggatagttcccactttcttgggaaaa 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 3921 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: join(1..2676, 3520..3918)
OTHER INFORMATION: /product= "xa-21"
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                   CTCTGCAACAACTTTCAGAGGGTCTCTTCCATCATCGTTGGGCAGGCTTAAAAACTTA 1278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (genomic)
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                                                                                                                                                                                                                                                                                                                             Score 57.4; DB 4;
Pred. No. 1.3e-06;
0; Mismatches 176;
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US-08-587-680A-3
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                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3921 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
ETILING DATE: 17-JAN-1995
PRIOR APPLICATION UNMBER: US 08/475,891
ETILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
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ADDRESSEE: Townsend
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Procedures and Materials for Conferring
                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                              NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                  LOCATION: join(1..2676, 3520..3918)
OTHER INFORMATION: /product= "Xa-21
                                                          NAME/KEY:
                                                                                                                  STRANDEDNESS:
TOPOLOGY: lin
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Song, Wen-Yuang
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SYSTEM: PC-DOS/MS-DOS
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                    "Xa-21"
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Query Match

5.28;

Score 57.4;

DB 4;

Length 3921;

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GENERAL INFORMATION:
APPLICANT: Ronald
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Patent No. 5859339
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INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
TOWNSEND and Townsend and Crew LLP
TERROR OF SEQUENCE ADDRESS:
TOWNSEND AND CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02370-058910US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 01
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE:
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                                                                       STRANDEDNESS:
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                                                                                                                                          ENGTH:
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                                                                                                     nucleic acid
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Song, Wen-Yuang
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                                            linear
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   DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US 08/373,375
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0; Mismatches 176;
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; LOCATION: join(512.
; OTHER INFORMATION:
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US-08-475-891A-3
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US-08-587-680A-24
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity Matches 163; Conserv
        CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-POS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,680 FILING DATE: 17-JAN-1996
                                                                                                                                                                                                                                                                         ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 27
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                              San Francisco
California
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Song, Wen-Yuang
Szabo, Veronique
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RMATION: /product= "RRK-B"
RMATION: /note= "Ra21 xanthomonas spp. disease
RMATION: resistance gene RRK-B from rice (Oryza
RMATION: sativa)"
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48.1%;
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Pred. No. 1.6e-06;
0; Mismatches 176;
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Best Local Similarity 49.0%;
Matches 150; Conservative
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FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-058:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1976-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
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COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                              NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
CONDRESSEE: Townsend and Townsend Khourie and C:
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                 TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE
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LABAVITCH, JO
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STOTZ, Henrik
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                                                                                                                                                                                                                                                                                             John M
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Pred. No. 1.6e-06;
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US-08-238-163-1
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                                                                                                                                                              sequence 1, Application US/08238163
Patent No. 5569830
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Best Local Similarity 50.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Bastian, Kevin L.
REGISTATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/238,163 FILING DATE: 03-MAY-1994
                                   APPLICANT: BENNETT, Alan
APPLICANT: LABAVITCH, John M.
APPLICANT: POWELL, Ann
APPLICANT: STOTE, Henrik
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
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               CORRESPONDENCE
                               NUMBER OF SEQUENCES:
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                                                                                                                                                  INFORMATION:
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(415) 543-5043
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Townsend and
               ADDRESS:
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Pred. No. 6.7e-06;
0; Mismatches 181;
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RESULT 10
US-08-567-375-15
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REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPHO: (415) 543-9643
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                          Sequence 15, Patent No. 5
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Best Local (
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APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
                                                                                                                                                                                         GENERAL INFORMATION:
               APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Wang, Wen-Yuang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 16
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MEDIUM TYPE: Floppy disk
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STRANDEDNESS: .single
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Similarity 51.5%;
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Townsend and Townsend and
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Pred. No. 1.2e-05;
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  Crew LLF
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US-08-473-553A-1
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; Sequence 1, Application US/08473553A
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
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APPLICATION NUMBER: US 01
FILING DATE: 07-JUN-1995
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APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
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MEDIUM TYPE: Floppy disk
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CITY: S:
STATE: (
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                                                                                                                                                                                                                                                                                                                                                                                           93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 CTGGTGCACTTCCTAGTGCTTTTGGAAACTATTCAGGGCTGAAGAATCTTGTGTTAACTG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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California
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Best Local Similarity 47.0
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 781-1
TELEFAX: (415) 398-324
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Flop COMPATIBLE
COMPUTER: FLOP POSSIBLE
COMPUTER: PATENT FO-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Meyerowitz
APPLICANT: Clark, Ste
APPLICANT: Williams,
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 5733 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Silva, Robin M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                                                                                                                                                        3482 GGGAGAACAATTTCACGTTACAATTACCGGCGAATCTTGGCCGGAACGGGAATCTAATAA 3541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                  3542 AGCTTGATGTCTCTGATAATCATCTCACCGGACTTATCCCCAAGGACTTATGCAGAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                             446
626 cacggcaatcccaagccttta 646
                                                                                                                                                                                                                                                                                                                   386 tctctggacatcttgcgcctgagcttgggaagcttgaacatttacagtatctagagctct 445
                                                                                                                                                                                                                                                                                                                                                                                          326 tccatgtcacctgtaaccaagacaaccgcgtcactcgtgtggatttgggaaattcaaacc 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                             gcttggatctgtacaacaaccatcttacagggatagttcccactttcttgggaaaattga 565
                                                                                                                                                                                                                                         acaaaaacaacatccaaggaactataccttccgaacttggaaatctgaagaatctcatca 505
                                                                                                                                                                                                                                                                                 TCTACGGACAAATACCAGAGGCCATCGGAGAATTACCAAAACTCGAAGTCTTCGAAGTAT
                                                         AGAAATTAGAGATGTTAATTCTCTCTAACAACTTCTTTGGTCCAATTCCAGAAGAGC
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2434..5037
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Pred. No. 0.00033;
D; Mismatches 170;
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Suite 3400
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3662 TTGGTAAATGCAAATCCTTAA 3682

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RESULT 12
US-08-232-463-14
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Best Local S
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Patent No. 56703
                                                                                                                                                                                                                                                                      Matches
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APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIAM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                               1233
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                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                   108
                                                                                                                                                                                                                                     48 ccctaattttgctttctcctctttgttcagaaaattttcccttttactctcaaaattccttt 107
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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                          cgaaggagatgctctctacgctcttcgccggagtttgacagatccagaccatgtcctcca
                                                               gctcttcgcagcttcgttaaccctaaccttagctttgattcacctggtcgaagcaaactc 227
                                                                                                                                                               tcgatttccctctcttaaacctccgaaagctcacatggcgtctcgaaactatcggtggga 167
                                                                                                                                                                                                                                                                     h 4.4%; Score 48.6; DB 1; Length 7218;
Similarity 3.5%; Pred. No. 0.00047;
12; Conservative 196; Mismatches 135; Indels 0
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22313-0299
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5169835-11
;Patent No. 5169835
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Best Local Similarity 55.2
Matches 80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US
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TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS
NUMBER OF SEQUENCES: 48
                                                            SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,644
FILING DATE: 06-JUN-1994
                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS: ADDRESSEE: Sally A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1933
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               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                             APPLICANT: Bergmann, Carl
TITLE OF INVENTION: Nucleotide Sequences Coding An
TITLE OF INVENTION: Endopolygalacturonase Inhibitor
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COUNTRY: US
ZIP: 80303
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FILING DATE:
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De Lorenzo, Giulia
Salvi, Giovanni
Albersheim, Peter
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06-DEC-1991
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               IT RM 91A 000915
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                                                                                                             Version
                                                                                                                 #
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FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sullivan, Sally A.

APPLICATION NUMBER: WO POSITION DATE: 04-DEC-1992

WO PCT/IT/00158

PRIOR APPLICATION DATA:

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; FEATURE:
; NAME/KEY:
; LOCATION:
; 08-08-244-646-16
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US-07-867-106-2/c
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TELEPAX: (303)499-8089
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      Sequence 2, Application US/07867106 Patent No. 5389526 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity Matches 117; Conserv
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 APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 19-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
ORGANISM: Pha
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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Pred. No. 0.025;
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Search completed: June 23, 2000, Job time: 40238 sec

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US-07-867-106-2
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Best Local (
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ETILING DATE: 19920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU DJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-588-3100
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COUNTRY: USA
COUNTRY: USA
ZIP: 19103
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO:
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LOCATION:
FEATURE:
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Maximum DB seq length: 1000000
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(without alignments)
723.220 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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REFERENCE AUTHORS

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2E 1 (bases 1 to 447)

2S Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H.,

McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,

Retzel, E. and Somerville, C.

Genes galore: a summary of methods for accessing results from

large-scale partial sequencing of anonymous Arabidopsis cDNA clones

AL Plant Physiol. 106, 1241-1255 (1994)

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115 c 83 g 126 t 17 others
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Retzel,E. and Somerville,C.
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Seq primer: T7 dye primer.
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MSU-DOE Plant Research Laboratory
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Pred. No. 1.4e-73;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                           on Sep 19, 1997 this sequence ver:
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, Retzel, E. and Somerville, C.
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31949 Lambda-PRL2
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Tel: 517-353-0854
Fax: 517-353-9168
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                                                                                                                                                                                                                                                                    il: 22313tcn@ibm.cl.msu.edu
primer: T7 dye primer.
    Location/Qualifiers
               103
         /note-"Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated eticlated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA. "

103 a 105 c 78 g 99 t 16 others
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/db_xref-"taxon:3702"
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                                                                                                                                                                               /clone_lib="Lambda-PRL2"
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AA394359.1
EST.
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Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H.,
Newman, T., deBruijn, F.J., Raikhel, N., Somerville, S., Thomashow, M.,
Retzei, E. and Somerville, C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
plant, Physiol. 106, 1241-1255 (1994)
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                                                                                                                                                                                                                                                                                                                     Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
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                                                                                                                                                                                                                                     Lansing,Mi
Tel: 517-353-0854
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                                                             /organism-"Arabidopsis
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                                                                                        thale cress.
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                       AI100680 336
33801 Lambda-PRL2
Arabidopsis.

1 (bases 1 to 336)

Newman, T., deBruijn, F.J., Green, P.,
McIntosh, L., Ohlrogge, J., Raikhel, N
Retzel, E. and Somerville, C.
Genes galore: a summary of methods
                                                                                                                                                                                                                                        sequence.
                                                                                                                                                                                                        AI100680.1
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114 c 125 g 126 t 18 others
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Pred. No. 5.3e-68;
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                                  Green, P., Ke
Raikhel, N.,
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   for accessing
                                    Keegstra,K.,
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                                  Kende, H.,
,S., Thomashow, M.,
   results from
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sequence.
AI100481
AI100481.1
EST.
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The sequence entry for this EST
is being submitted in the sense
Seg primer: M13-21.
                                                                           34856
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Tel: 517-3
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Fax: 517-353-9168
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09 a 55 c 70 g 99 t 3 others
                                                                         181 442
Lembda-PRL2
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/strain="var columbia"
/db_xref="taxon:3702"
/clone="179J19xp"
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Pred. No. 9.1e-68;
0; Mismatches 3;
                                                                             thaliana
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orientation
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                                                                           CDNA
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90J7XP 3',
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atcatctggtctcaattgagaacttcgaggtc--tgtatgtaaaatttctaaatgcgatt
                                                                                                                                                                                                                                                                                     tttgctcacattcctttacagaactttgagaaccaacccgagattgg--agggaccggaat 760
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                                                      CTATGTAATAAGTATATATGTAGTCCAA - - AAAAAAAATGAAGAATCGAATCAGTAAT
                                                                      ttatgtaataagtatatatgtagtaaaaaacaaaaaaaatgaagaatcgaatcggtaat
                                                                                                                                                                                                                                                                    397;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lansing, Mi
Tel: 517-353-0854
Fax: 517-353-9168
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: 22313tcn@ibm.cl.msu.edu
The sequence entry for this EST has been reverse complimented
is being submitted in the sense orientation.
Seq primer: M13_Universal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McIntosh,L., Ohlrogge,J., R Retzel,E. and Somerville,C.
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1 (bases 1 to 442)
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                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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/Clone_lib="Lambda-PRL2"
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Note: lambda Zip-Lox; Note: lambda Zip-Lox; Alpha Same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The CDNA inserts were directionally cloned with Sal-Not arms using coligo dT primed cDNA."
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/strain="var columbia"
/db_xref="taxon:3702"
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Pred. No. 1.5e
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Raikhel, N.,
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,S., Thomashow,
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acaaaaaaatgaagaatcgaatcggtaatatcatctggtctcaattgagaacttcgagg 970
                                                                                                                             GCACCTGAAACAACTGGCAAAACCTGAAAATGAAGAATTGGGGGGGTGACCTTGTAAGAAC
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ATTS3221 Versailles-VB
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Route de Saint-Cyr,78026 Versailles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thierry@versailles.inra.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Versailles-VB"
/tissue_type="whole seedlings"
/dev_stage="in vitro-grown etiolated seedlings,5 days old"
/note="Vector: pBluescript"
/note="Vector: pBluescript"
62 c 65 g 119 t 1 others
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/strain="ecotype Columbia"
/db_xref="taxon:3702"
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cactaactgcacctgaaacaactggcaaaaacctgaaaaatgaagaattggggggtgacctt 842
                                         CACTAACTGCACCTGAAAAAATTGGCAAAACCTGAAAATGAAGAATTGGGGGGGTGACCTT 120
                                                                                                                                                                                                                 346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow, Retzel,E. and Somerville,C.
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33806 Lambda-PRL2 Arabidopsis thaliana
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The sequence entry for this EST
is being submitted in the sense
Seq primer: M13-21.
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1 (bases 1 to 360)
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Tel: 517-353-0854
Fax: 517-353-9168
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Michigan State University
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                                                                                                                                                                                                                                                                                                                                      /note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dr primed cDNA.

77 g 105 t 2 others
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/strain="var columbia"
/db_xref="taxon:3702"
/clone="90J7XP"
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                                                                                                                                                                                                                                 Score 316; DB 42;
Pred. No. 8.3e-64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E. and Somerville,C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones plant Physiol. 106, 1241-1255 (1994)
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primer: T7 dye primer.
                 98
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               oligo dī primed cDNA.
1 85 c 67 g
                                    /note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using olligo off primed cDNA."
                                                                                                                                                                                                                               /organism="Arabidopsis
/strain="var columbia"
/db_xref="taxon:3702"
/clone="179J19T7"
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95148729
On May 5, 1995 this sequence version re Contact: Thomas Newman
MSG-DOE Plant Research Laboratory
Michigan State University
MSG-DOE-PRL, Michigan State University
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                                                                                                            Email: 22313tcn@ibm.cl.msu.edu
The sequence entry for this Est
is being submitted in the sense
Seq primer: M13-21
                                                                                                                                                           Lansing, Mi
Tel: 517-353-0854
Fax: 517-353-9168
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
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/organism-"Arabidopsis
/strain-"var columbia"
/db_xref-"taxon:3702"
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                                             /clone="187H5XP"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; eudicotyledons; core
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
euphyllophytes; Rosidae; eurosids II; Brassicales; Brassicaceae;
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234606
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                                                                           Laboratoire de Biologie Cellulaire
Route de Saint-Cyr,78026 Versailles
Email: thierry@versailles.inra.fr.
Location/Qualifiers
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80 c 70 g 99 t 2 others
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/organism-"Arabidopsis thaliana"
/strain-"ecotype Columbia"
/db_xref-"taxon:3702"
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                                                                                                                                                 On May 5, 1995 this sequence version
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
                                                                                                                                                                                                                                Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clone Physiol. 106, 1241-1255 (1994)
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        11: 517-353-0854

IX: 517-353-9168

Bail: 22313tcnellbm.cl.msu.edu

Resequence entry for this EST has been reverse

being submitted in the sense orientation.

9 primer: M13-21.
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Lambda-PRL2
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/clone_lib="Versailles-VB"
/tissue_type="whole seedlings"
/dev_stage="in vitro-grown etiolated seedlings,5 days old"
/note="Vector: pBluescript"
- 98 c 60 g 105 t 1 others
Location/Qualifiers
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                                                 Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C.

Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
On May 8, 1995 this sequence version replaced g1:801143 Contact: Thomas Newman
                                                                                                                                                            Arabidopsis.

1 (bases 1 to 336)
                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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H37296
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110 a 74 c 66 g 93 t 5 others
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/db_xref="taxon:3702"
/clone="185LlXP"
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/organism="Arabidopsis
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Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
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Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
                                                                                                                                   AW443205 608 bp mRNA EST EST308135 tomato mixed elicitor, BTI Lycopersicon clone cLET43M10 5', mRNA sequence.
Lycopersicon.

1 (bases 1 t
                        Lycopersicon esculentum Eukaryota; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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/strain="var columbia"
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                                                 AAGCTAACAGGACCAATCCCAAGAGAACTTACTAGCATTTCTAGCCTGAAAGTTGTGGAT
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                                                                   cgattgaccggtccaatcctagagcactcacggcaatcccaagcctttaaagttgttgac
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Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
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Clemson University Genomics Institute
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100 Jordan Hall, C
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95; Conservative
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/cultivar="Rio Grande PtoR"
/db_xref="taxon:4081"
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/tlssue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XL1-Blue_MRF',"
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0; Mismatches 180;
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Maximum DB seq length: 1000000
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58: gb_htg14:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Ω იი G ი Score Query Match 0.4 1815 4604 8.5 101284 8.3 181513 8.2 112529 8.2 112529 8.1 1100887 8.1 116944 8.0 5033 7.9 10835 7.9 10835 7.1 13384 7.7 142418 7.7 13384 7.7 13384 7.5 6694 7.5 6694 8 184440 8 1142418 7 1133840 5 6695 5 6695 5 3176 5 3176 5 3178 6 3178 1 98471 1 1947 1 11945 Length DB 8885885878750 8885885878750 LELRPGENE ATACO09991 ATACO11765 ATACO11765 ATACO11620 ATACO11620 AC008017 INUT988 AC005957 AB010075 AB010075 AP000815 AC003981 AC003981 AC003981 AC003981 AC003981 AC003981 AC003981 AC003981 AC003981 AC003981 AC003981 AB029327 E12705 ATU47029 F15P11 A67815 AC012654 AB010698 OSU72724 AIF17061 SBU62279 DCU93048 A67797 U42444 OLRKLP2 ATF1C12 OLRKLP1 AB019227 SBRLK1 A57133 AF053996 U42445 A57130 A67817 A67817 A67825 A67821 A67823 A67823 x95269 L.esculentu x95269 L.esculentu AC009991 Arabidops AC021198 Arabidops AC0211965 Arabidops AC011546 Arabidops AC011546 Arabidops AC011546 Arabidops AC011547 Arabidops AC0115957 Arabidops AC005957 Arabidops AC005957 Arabidops AC005957 Arabidops AC005957 Arabidops AC005957 Arabidops AC005957 Arabidops AC005957 Arabidops AC005957 Arabidops AC012654 Arabidops AC012654 Arabidops AC012654 Arabidops AC012654 Arabidops AC012654 Arabidops AC012654 Arabidops AC012774 Arabidops AC012774 Arabidops AC012774 Arabidops AC012775 Oryza longi AB01927 Arabidops AC012775 Oryza longi AB01927 Arabidops AC012775 Arabidops AC012775 Oryza longi AB01927 Arabidops AC012775 Oryza longi AB01927 Arabidops AC013775 Oryza longi AB01927 Arabidops AC013775 Oryza longi AD012725 Oryza longi AL02725 Oryza longi AL027254 Arabidops AC012725 Oryza longi AL027275 Oryza longi AL027274 Arabidops AC012725 Oryza longi AL027274 Arabidops AC012725 Oryza longi AL027274 Arabidops AC0127275 Oryza longi AL027274 Arabidops AC012725 Oryza longi AL027274 Arabidops AC012744 Arabidops AC012744 Arabidops AC012744 Arabidops AC012744 Arabidops AC012744 Arabidops AC012744 Arabidops AC012744 Arabidops AC012744 Arabidops AC012744 Arabidops AC0 A67819 Sequence 24 A67817 Sequence 22 A67825 Sequence 30 A67821 Sequence 26 A67823 Sequence 28 A67827 Sequence 32 U62279 Sorghum bic U93048 Daucus caro A67727 Sequence 2 Description

ALIGNMENTS

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De, V.S., Scher
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De, V.S., Schmidt, E.D., Van, H.G. and
PRODUCTION OF APOMICTIC SEED
PATENT: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
                                                                                                                                                                                                                                                                         unidentified unclassified
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1 (bases 1 to 1063)

De, V.S., Schmidt, E.D., Van, H.G. at PRODUCTION OF APOMICTIC SEED Patent: WO 9743427-A 20-NOV-1997;

CIBA GEIGY AG (CH)
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De, V.S., Schnidt, E.D., Van, H.G. a
PRODUCTION OF APOMICTIC SEED
PATENT: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
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1 (bases 1 to 2089)

1 (bases 1 to 2089)

De, V.S., Schmidt, E.D., Van, H.G. and PRODUCTION OF APOMICTIC SEED Patent: WO 9743427-A 20-NOV-1997;
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PPFFTQPPPVSTPSGYGITGALAGGVAAGAALPFAAPALAFARAGTLVAVRRLse
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GGTTCGATTCCAGAAACACTAGGCAACCTGACTAATCTCATCAGCTTGGATCTCTGGGAC
                                                                                             cctgagcttgggaagcttgaacatttacagtatctagagctctacaaaaacaaccatccaa
                                                                                                                                                 AACAATAACTTTGTCATCCGCGTGGATTTGGGCAATGCAGGCATCTCCGGTCCTCTGCTT
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                                 ggaactataccttccgaacttggaaatctgaagaatctcatcagcttggatctgtacaac 484
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Lillopsida; Poales;
Poaceae; Sorghum,
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Sorghum bicolor leucine-rich
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2 (bases 1 to 936)
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nilarity 58.5%;
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/gwngtlanpotwehytcnnnwevirvdlgnagisgpllpdlaeignloyielyggl
ngsipetlgnltnligldlwdnlltgeipttlgsystlrylrlygnultgpipssegn
LTSLLESKLQENSLSGA LPASLGNIKALQESRLNDNMLTGTVPSKSEPLSTEGNLTEL
NTDRNNLDGTRTSSGLRYTAIIQDALKTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="protein-protein ligand binding"
/note="leucine-rich repeat-containing extracellular
glycoprotein; contains six N-glycosylation sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental 232 c 207 g 250 t
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/db_xref="GI:1710124"
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/db_xref="taxon:4558"
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                                                                                                                                                                                                                                                                                                                                                                     Score 156.6; DB 8;
Pred. No. 1.6e-28;
0; Mismatches 194;
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47907, USA
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υ93048.1
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Direct Submission
Submitted (12-MAR-1997) Molecular Biology, Agricultural University
of Wageningen, Dreyenlaan 3, Wageningen 6703 HA, The Netherlands
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schmidt,E.D., Guzzo,F., Toonen,M.A. and de Vries,S.C.
A leucine-rich repeat containing receptor-like kinase marks somatic plant cells competent to form embryos Development 124 (10), 2049-2062 (1997)
97313247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
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Schmidt, E.D.L., Guzz
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      Conservative
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34. .1695
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   Score 101.8; DB 8; Pred. No. 5.1e-15; 0; Mismatches 162;
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   AAGTGGACCAATTCCTAGTGATCTTGGGAATCTGACAAATTTGGTGAGCTTGGACCTATA
                                                                       TGATGCTTACCTTGACAAATATGGGGGTTCTTATGACATTGGAGCTTTACAGCAATAACAT 197
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A67797.1 GI:4756623
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De, V.S., Schmidt, E.D., Van, H.G. and Hecht, V.F.
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//db_xref="G1:4756324"
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//tanslation="murssinilinymoftdayidkygylmtlelysnnisgpipsdlg
NLTNLYSLDLYMNSFSGPIPDTLGKLTRLEFLRINNNSLSGPIPMSLTNITTLQVLDL
SNNRLSGPYDDNGSFSLFFPISFANNLKICGFYTGREOFGSFPFSPPPPFIPPSTVOP
PGONGPTGAlaGGYAAGAALTAAPANAAFAWWRAKREPEHFTDVPAEEDFWHLGGUK
RFSLRELQVATDTFSTILGRGGFGKVYKGRLADGSLVAVKRLKEERTPGGELQFQTEV
EMISMAVHRULLRLRGFCMTPTERLLYTPYMANGSVASCLRERQPSEPFLDMFTRKRI
ALGSARGLSYLHDHGDFKIHRDVKAANILLDEEFERVYGDFGCLAUMDYKDTHVTTA
VRGTLGYIAPEYLSTGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDMV
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2 (bases 1 to 4604)

Tornero, P., Mayda, E., Gomez, M.D., Canas, L., Conejero, V. and Vera, P. Characterization of LRP, a leucine-rich repeat (LRR) protein from tomato plants, that is processed during pathogenesis
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/cultivar="vFN8"
/db_xref="taxon:4081"
/tissue_type="leaf"
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/gene="LRP"
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                                      Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Haas,B., Ronning,C.M., Koo,H., Fujil,C.Y., Utterback,T.R., Barnstead,M. Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome III BAC F9F8 genomic sequence unpublished
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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                                                                                                        Barnstead, M.E.,
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tigr.org/tdb/at/at.hml).

Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity are named as 'unknown' proteins. Genes without protein programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RW/RepeatMasker.html). Regions of genomato sequence that are not annotated as genes but have predicted exons by GRAIL are annotated as misc features.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e-mail: xlin@tigr.org
BAC clone F9F8 is from Arabidopsis chromosome III and is near the
molecular marker 94547.
The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (08-OCT-1999) The Institute for Genomic Research,
Medical Center DT., Rockville, MD 20850, USA
On Oct 8, 1999 this sequence version replaced gi:5902413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (09-SEP-1999) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org 3 (bases 1 to 101284)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prediction programs including GRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), and NetPlantGene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Dr. Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes were identified by a combination of three methods: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="exc
124. .259
/note-"exon predicted by xgrail, complement(2090. .2250) /note-"exon predicted by xgrail,
                                                                                                                         complement(1516...1694)
/note="exon predicted b
excellent_shadowexon"
                                                                                                                                                                                                                                                                     /note="exon predicted 854..973
                                                                                                                                                                                                                                                                                                           /note="exon predicted by 672. .752
                                                                                                                                                                                                                                                                                                                                                 excellent_shadowexon"
355. .594
                                                               /note="exon predicted by 1747. .1838
                                                                                                                                                                                    /note="exon predicted by marginal_shadowexon"
                                                                                                                                                                                                                              /note="exon predicted by xgrail,
complement(1182. .1357)
                                                                                                                                                                                                                                                                                                                                                                                                             complement(347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:3702"
/chromosome="III"
/map="g4547"
                                                                                                                                                                                                                                                                                                                                                                                       /note-"exon predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                /note="exon predicted by xgrail,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis thaliana"
/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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/note="exon predicted by xgrail, qual complement(2975. .3024)
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join(3070. .3325,3565. .3642,4094. .44506. .4655,4800. .>5013)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(5696.
7467. .772
                                                                                                                                                                                                                                                                          /gene-"F9F8.3"
/note-"similar to leucoanthocyanidin dioxygenase GB:BAA20143 [Perilla frutescens] "
complement(join(9426. .9674,10198. .10528,11098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLSVSFYFGARLNRNERKRLFSLINDLPTLFDVVTGRKAMKDNKPSSDSGSKSRNGTK
RSIDGQTKSSTPKLMEESYEEEEEEEDEHGDTLCGSCGGHYTNEEFWICCDVCERWYHG
KCVKITPAKAESIKQYKCPPCCAKKGRQ"
complement(7717. .7760)
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5589. .7932
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complement(5513..5597)
/rpt_family="(GA)n"
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/DICCEID_Id-"AAF01505.1"
/DLAXTEFF*GI: 6016678"
/TLAGNSIA-LION-"MYGPARFOTULEGSSIVQMSFGHGGWGAILSEVYARKADIILRG
YYGMNSSRALEVVDQVFFKDAAVQPSLVIVYFGGNDSMAPHSSGLGPHVPLTEXVDNM
KKIALHILQSLSDFTRIIFLSSPPVDEAKVRQNQSPYLSEVIRTNDLCKTYSDACVELC
QELGLEVVDLFSTFQKADDWKTYCFTDGIHLSAQGSKIVAGEILRVVKEAEWHPSLHW
                                                                                                                                                                                                                                                                                                                                                             complement(<9426. .>11865)
/gene="F9F8.3"
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8515. .8572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="G1:6016679"
/translation="MAAAAVSSNPRTVEEIFKDYSARRAALLRALTKDVDDFYSQCDP
EKENLCLYGHPNESWEVNLPAEEVPPELPEPALGINEARDGMQRKDWLSLVAVISDCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to nucleic acid binding protein Alfin-1
GB:AAA20093 [Medicago sativa]"
join(5696. .5795,5897. .5929,6013. .6235,7264. .7387,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="r9F8.1"
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thaliana'"
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LFSGNEDDKKRISEACREMGFGVVINHGVKPELIMDAARETWKSFFNLPVEAKEVYSKE
PRIVEGYGSELGVEKGAILDWNDYYLHFLPLALKDFWKWFSLPSNIREMNDEYGKEL
VKLGGRLMTILSSNIGLRAEQUQEAFGGEDVGACLRVNYYPKCPQPELALGLSPHSDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(7810. .7847)
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/note="unknown protein"
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/protein_id="AAF01506.1"
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506. .4655,4800. .5013)
GGMTILLPDDQVVGLQVRHGDTWITVNPLRHAFIVNIGDQIQILSNSKYKSVEHRVIV
                                                                                                                                                                                                                                      /gene="F9F8.
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lement(join(<9426. .9674,10198. .10528,11098.
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                                                                                                                                                                                                                                                                                                                 tccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGAGGTTGTCTGCTTTATTACTTTCCCACAATCAGTTCACAGGCACGATTCCTAATAACA 44697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTTACAGGTTGATTCCAATAAGCTCAGTGGAAATGTTCCCCATCTCACTACTGAATTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                              tcacggcaatcccaagccttaaagttgttgacgtctcaagcaatgatttgtgtggaacaa
                                                                                                                 Arabidopsis
thale cress
                                              AC021198.2
                                                                                             sequence.
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complement(13367. .13468)

/note="exon predicted by xgrail, quality marginal"

complement(13742. .13788)

/note="exon predicted by xgrail, quality marginal"

/note="exon predicted by xgrail, quality marginal"

complement(join(13822. .14179,14261. .14398,14502. .1458.

14676. .14861,14941. .15033,15124. .15190,15272. .15361,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MANLVLSECGIPPLPRIYTTPRSNFLSNNNKFRPSLSSSYKTS
SSPLSFGLNSRDGTTRWALLWSTPLTTPIFESSPLEEDNKQRFRPFFNLADIF
RAIFKHCWYKNPWKSLSYVVRDVAIVFALAAGAAYLNWIUWPLYWLAAGFMFWALFV
LGHDCGHGSFSNDFKLMSVVGHLLHSSILVPYHGWRISHRTHHONHGHYENDESWHFM
SEKIYNTLDKPTRFFRFTLPLVMLAYPFYLWARSPGKKGSHYHPDSDLFLPXERKDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(13988. .14179,14261. .14398,14502. .14582, 14576. .14861,14941. .15033,15124. .15190,15272. .15361,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="identical to omega-3 fatty acid desaturase, chloroplast precursor GB:P46310 [Chloroplast Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(13822. .16380)
/gene="F9F8.4"
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/gene="F9F8.4"
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/db_xref="GI:6016681"
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Local Similarity 54.1%;
                                                                                                                                                                             cactcacggcaatcccaagccttaaagttgttgacgtctcaagcaatgatttgtgtggaa 644
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                                                                                                                               CCTTCGGAAATCTCAAGAACTTGACGTATCTTTATCTTTACCTGAATTATTTAACTGGTG 2765
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Liu,S.X., Sakano,H., Yu,G., Lee,J.M., Lenz,C., Pham,P., Torium,Chin,C., Chiou,J., Choi,E., Chung,M., Gonzalez,A., Howng,B., Chin,C., Chiou,J., Rim,C., Law,B., Miranda,M., Brooks,S., Buehler,E., Chao,Q., Conn,L., Conway,A.B., Hansen,N.F., Johnson-Hopson,C., Khan,S., Kim,C., Lam,B., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Sonthwick,A., Davis,R.W., Ecker,J.R., Federspiel,N.A. and
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/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="1"
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1. .81513
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Pred. No. 5.6e-10;
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                                                                                                                                                                                                                                                                                                                    http://gnomic.stanford.edu/-chris/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tlgr.org/tdb/at/at.html).

Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding trNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Regions of genomic sequence that are not annotated as genes but have predicted exons by CRAII, are annotated as genes but have predicted exons by CRAII, are annotated as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor factor as minor f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-DEC-1999) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA On Dec 8, 1999 this sequence version replaced gi:6102640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lin,X. and Kaul,S.
Direct Submission
Submitted (14-OCT-1999) The Institute for Genomic Research,
Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Haas,B., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome I BAC F1M20 genomic sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous if from arthur.epm.ornl.gov), Genefinder (Phil Green, University Washington), Genscan (Chris Burge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAC clone F1M20 is from Arabidopsis chromosome I and is near the molecular marker m1425.
The orientation of the sequence is from SP6 to T7 end of the BAC
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The Institute for Genomic Research
9712 Medical Center Dr.
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e-mail: xlin@tigr.org
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                                                                                                                                                                                                                                                                                                         exons by GRAIL are annotated as misc features
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/cultivar-"Columbia"
/db_xref-"taxon:3702"
/chromosome-"I"
                                                            /map-"m1425"
                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                          .134402
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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to dolichyl-phosphate mannosyltransferase polypeptide 2 08:450365 [Homo sapiens] (regulator of dolichol phosphate-mannose synthesis: EMBO J 1998 Sep 1;17(17):4920-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNVAGEAIHGWVPLRSDAFEKLEKIGQGTYSNVFRAVETETGRIVALKKVRFDNFEPE
SVKFMAREILILRRLNHPNIIKLEGLITSKLSCNIQLVFEYMEHDLTGLLSSPDIKFT
TPQIKCYMKQLLSGLDHCHSRGYMHRDIKGSNLLLSNEGILKVADFGLANFSNSSGHK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="exon predicted by xgrail, quality marginal" complement(join(<1655. .1777,1908. .2135,2258. .2581, 2679. .2963,3052. .>3429))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="exon predicted by xgrail, quality good_shadowexon"
complement(1509..1530)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="exon predicted by xgrail,
complement(1356. .1475)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="exon predicted by xgrail,
complement(744. .1286)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="exon predicted by xgrail, quality excellent"
complement(393. .453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(4069. .4131)
/note-"exon predicted b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HKRGTASSALVSQYFTTKPFACDPSSLPIYPPSKEIDTKHRDEAARSVISFIT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKPLTSRVYTLWYRPPELLLGATDYGASYDLWSYGCVFAELLLGKPILRGRTEVEQLH
KIFKLCGSPPEDYWKKSKLPHAMLFKPQQTYDSCLRETLKDLSETEINLIETLLSIDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(<1655. .>3429)
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                                                                                                                                                                                                                                                                                                                              /note="exon predicted by xgrail, quality excellent"
complement(<5342. .>7603)
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PQDYAILVPYFAGIALLSLISYFIGMVMLKSKKKKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(<4608. .>4974)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="exon predicted by xgrail, quality excellent"
complement(join(<4608. .4760,4885. .>4974))
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/gene="F1M20.3"
                                                                                                                                                                                                                                                                         complement(<5342. .>7603)
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                          /product="putative type II intron maturase"
/protein_id="AAF15907.1"
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                                                                                                                                                                                                                      /note≖"contains Pfam profile: PF01348 Type II intron
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polypeptide 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="F1M20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="f1M20.2"
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                                                                                                                                                                                                                                                                                                                                                                                       lement(5111.
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                                                                                                                                                                                                                                                                                                                                                                                             .5190)
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CDS

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misc_feature
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/gene="F1M20.4"
/noq2...>14231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLKKRVKEQCINGKFSDLLKKVIARPETLRDAYDCIRLNSNVSITERNGSVAFDSIAE
ELSSGYFDVASNIFSIVARDKYKEYLVLPSVALKVVOŒAIRYVEVPESPHFSKISHS
CRSGRGRASALKYINNISKRSDWCFFIJSLNKKLDVSVERULSYMEERVEDSSLSILL
RSMFEARVLNLEFGGFPKGHGLPQEGVLSRVLMIYLDRFDHEFYRISMRHEALGLDS
KYDEDSPGSKLASWFRRQAGEQGLKSTTEQDVALRVYCCRFMDEIYFSYSGFKKVASD
IRSEAIGFLRNSLHLDITDETPDFSCEATSGLRVLGTLYKNVRESPTYKAVHKLKEK
VRLPALQKEEAMFLGTVSIGKKNLGHGLKKVKSEIKGLADSNSTLSQLSCHRKARAK
TDHWYKILLRINMEDVLRTSADRSEEFYLSKHVEPTYPQELKDAFYKEQNAAAXYVS
SETANLEALLPCPQSHDRPVFFGDVVAPTNAIGRRLYRYGLITAKGYARSNSMILLLD
TAQIIDWYSGLVERWYINYEGCSNFDEIKALINQIRNSCIRTLAKKYRIENBEIEKR
TDLELSTIPSAABDIEQDFQHEKLDSPAPDRDEHLTYGLSNSGLCLSLARLVSESSRPC
TOHWYSGLVERWYINYEGCSNFDEIKALINQIRNSCIRTLAAKKYRIENBEIEKR
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TAQIIDWYSGLVERWYINYEGCSNFDEIKALINGIRNSCIRTLAAKKYRIENBEIEKR
TADLELSTIPSAABDIEQDFQHEKLDSPAPDRDEHLTYGLSNSGLCLSLARLVSESSRPC
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NLSTNNFTGR1DD1FNGCRNLKYVDFSSNRFSGEVATGFGRLVEFSVADNHLSGN1SA 
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SMFGROCTLOMLDLSGNAFGGEFPGOVSNCONLNVLNLMGNRFTGN1FAE1GS1SSLK 
GLYLGNNTFSRD1FETLLLTRLVFLDLSRNKEGGD17GE1FGRFTOVKYLVLHANSYV 
GG1NSSN1LKLFNLSFLDLGYNNFSGQLFTE1SO1GSLKFLILAYNNFSGD1FOEYGN 
NPGCQALDLSFNKLTGS1FASFGKLTSLLMALANNSLSGE1FRE1GNCTSLLMFNVA 
NNOLSGREFBELTRMGSNFSFTFEVNRONKDK1IAGSGECLAMKRWIFAEFFPFNFVY 
A1ITKKSCRSLMPHYLKGYGLFFVCSAGSTVRTIK1SATLQLSGNKFSGE1PASISON 
DRLSTLHLGFNREFGKLJPE1GOLPLAFLNLTNNRFSGE1PADEIGNLKCLDSFN 
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DRLSTLHLGFNREFGKLJPE1GOLPLAFLNLTNNRFSGE1PADIGNLKCLDSFN 
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OSGNNTRKISNQVLGNRERTLLLIWISLALALAFIACLUVSGIVLAVVKASREAEIDL
LDGSKTRHDMTSSSGGSSPWLSGKIKLDKSTETALAMAFGATENESEETELYGRGLY
GTVYEGVLLDGREWAVKKLQREGTEAKKEFRAEMSTETASAMAFGATEHHECVPSIVHRD
DGSKKILVHEYMGGGSLEELITDKTKLQWKKRIDIATDVARGLYFLHHECVPSIVHRD
VKASNVLLDKHGNARVTDEGLARLLNVGDSHVSTVIAGTIGYVAPEYGQTWQATTRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="similar to brassinosteroid insensitive 1 GB:AAC49810 (putative receptor protein kinase); contains Pfam profiles: pr00550 Leucine Rich Repeat (17 repeats), pr00069 Eukaryotic protein kinase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QISLQAVDFGAWR"
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<10992. .>14231
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10574. .106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   marginal_snadowexon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCFVIGCSMAAPAVYTLHAMERQKFPGWKTGFSVCIPSSLNGRRIGLCKQHLKDLYIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="exon predicted
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                                 GTTTGAAGTTCTTGATTCTTGCTTATAATAACTTCAGTGGCGATATACCACAGGAGTATG
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AC015446/c
BASE COUNT
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Direct Submission
Submitted (16-NOV-1999) DNA Sequencing and Technology Center, Submitted (16-NOV-1999) DNA Sequencing Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Altafi, H., Nguyen, M., Lam, B., Southwick, A., Miranda, M., Brooks, S., Buehler, E., Chao, Q., Chin, C., Chiou, J., Choi, E., Gonzalez, A., Howng, B., Johnson-Hopson, C., Khan, S., Kim, C., Koo, T., Lee, J.M., Lenz, C., Liu, A., Liu, S., Mukharsky, N., Pham, P., Sakano, H., Shinn, P., Toriumi, M., Vaysberg, M., Yu, G., Ecker, J., Theologis, A.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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AC015446.2 GI:6692247
HTG: HTGS_PHASE1.
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Arabidopsis thaliana chromosome I clone
PROGRESS ***, 4 unordered pieces.
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                                                                                                                                                                                                                                                                                                               n Jan 12, 2000 this sequence version replaced gi:6437511. NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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50806: gap of unknown length
112529: contig of 61723 bp in length.
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  others
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** SEQUENCING
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1 (bases 1 to 100887)
1.11, X., Kaul, S., Town, C.D., Benito, M., Creasy, T.H.,
Ronning, C.M., Koo, H., Fujii, C.Y., Utterback, T.R., B.
Bowman, C.L., White, O., Nierman, W.C. and Fraser, C.M.
Arabidopsis thaliana chromosome III BAC F18C1 genom.
                                                                                                                                                                                                                                                                                                                                                                               Lin, X. and Kaul, S.
Direct Submission
Submitted (08-OCT-1999) The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Arabidopsis thaliana
                Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ft from arthur.epm.ornl.gov), Genefinder (Phil Green, University
                                                                                                                                                                                                    Submitted (18-JAN-2000) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA On Jan 18, 2000 this sequence version replaced gi:6175135. Address all correspondence to:at@tigr.org
                                                                                                                                                                                                                                                                                                                        Medical Center Dr, Rockville, MD 20850, USA, xling 3 (bases 1 to 100887)
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                                                                                                                                    BAC clone F18C1 is from Arabidopsis chromosome III and is near the molecular marker \min 172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                                                                                               The orientation of the
                                                                                                                                                                                                                                                                                                 Direct Submission
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53.9%;
  Genscan (Chris Burge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 80; DB 44; I
Pred. No. 1.3e-09;
0; Mismatches 140;
                                                                                                               sequence is from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
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PIN 18-JAN-ZVVV F18C1 genomic sequence,

86385

506 86505

86565

SP6 to T7 end of the BAC

v ftp

nomic Research, xlin@tigr.org

genomic

., Haas,B., Wu,D Barnstead,M.E.,

Wu, D.,

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FEATURES
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                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
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Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html).

Location/Qualifiers

Inceation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://gnomic.stanford.edu/~chris/GENSCANW.html), and NetPlantGene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIGLSIHRSPSVITPALRTIGNIVTGNDSQTQHIIDLQALPCLVNLLRSVNKTIKGK
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join[15397. 15585,16169. 16247,16449. .16543,16641. .16772,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                          complement(19632. .>21871)
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ement(14500
                                                                                                                                                                                                                                                                                                                                                                                    family="(GAA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(28290. .28335,28744. .29013,29330.
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В Ş B Š Š Š 밁 ş 밁 δÃ 밁 Query Match 8.1%; Score 79.8; DB 50; Best Local Similarity 53.3%; Pred. No. 1.4e-09; Matches 188; Conservative 0; Mismatches 147; 55747 55687 ACCTITCTCGACCTATCTACTAACAATTTTGTTGGTGAAATCCCTTCTTTTTGGCAGT 55746 55627 55567 AACTTCAGTGGTTGGATTCCTTCTTCCCTTGGAAACCTTTTTCACCTCACCTCTCCCAC 55626 55867 ACCCTTCCTCAAC 55881 524 ttgaagtctctggtctttttacggcttaatgacaaccgattgaccggtccaatccctaga 583 464 344 aacctctctggacatcttgcgcctgagcttgggaagcttgaacatttacagtatctagag 403 atcagcttggatctgtacaacaatcattacagggatagttcccacttctttgggaaaa 523 acaatcccaacaaac 658 TTGAACCAATTGTCTATTTTACGTCTTGATAATAATAAGCTTAGTGGTAACCTCCCACTT 55806 Length 100887; Indels 0; Gaps 0,

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O. longistaminata
CF-5 pathogen resi
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O. longistaminata
O. longistaminata
CF-5 pathogen resi
Maize Xa21 gene DF
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Daucus carota SERK
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Arabidopsis thalia
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Arabidopsis steroi
Tomato Xa21 clone
Tomato pathogen re
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20-NOV-1997.

13-MAY-1997; E02443.

R 14-MAY-1996; GB-010044.

N (NOVS) NOVARTIS AG.

I De Vries SC, Hecht VFG, Schmidt EDL, Van Holst OR WPI; 98-086529/08.

P-PSDB; W47019.

PF Production of apomictic seeds - useful in pla PF Production of apomictic seeds - useful in pla PS Claim 28; Pages 75-77; 123pp; English.

CC The sequence is that of an EST clone showing SERK LRR (leucine-rich repeat) sequences.

CC SERK LRR (leucine-rich repeat) sequences.
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V06587;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST clone.
receptor kinase; apomixis; apomictic; seeds; produc
plant breeding; leucine-rich repeat; ss.
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V06585

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Total number

of.

satisfying 1000000

chosen

parameters:

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Post-processing:

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summaries

Database

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score Pred.

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SUMMARIES

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Scoring table: Sequence: Title:

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GenCore version Copyright (c) 1993 - 2000

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v06586;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST cl
receptor kinase; apomixis; apomictic; seeds; pr
plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
Key
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Matches 885
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20-NOV-1997.
13-MAY-1997; E02443.
14-MAY-1996; GB-0100
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The sequence is that of an EST clone showing high homology SERK LER (Leucine-rich repeat) sequences.
Sequence 1063 BP; 313 A; 242 C; 206 G; 302 T;
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(NOVS ) NOVARTIS AG.
De Vries SC, Hecht VFG,
WPI; 98-086559/08.
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Pred. No. 8.9e-224;
0; Mismatches 32;
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D 20-NOV-1997.

E 13-MAY-1997; E02443.

F 13-MAY-1996; GB-010044.

R 14-MAY-1996; GB-010044.

R (NOVS) NOVARTIS AG.

De Viles SC, Hecht VFG, Schmidt EDL, Van Holst GJ;

R PP. 085529/08.

R P-PSDB; W47020.

R P-PSDB; W47020.

T Production of apomictic seeds - useful in plant breeding Claim 28; Pages 79-80; 123pp; English.

CClaim 28; Pages 79-80; 123pp; English.

CThe sequence is that of an EST clone showing high homology to SERK LRR (leucine-rich repeat) sequences.

Sequence 788 BP; 234 A; 191 C; 156 G; 207 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 757; Conserv
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V06588;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous ES
receptor kinase; apomixis; apomictic; seeds
plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
Key
CDS
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                                                                  agtttgacagatccagaccatgtcctccagagctgggatccaactcttgttaatccttgt 280
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tcaaacctctctggacatcttgcgcctgagcttgggaagcttgaacatttacagtatcta
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96.8%;
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Pred. No. 3.3e-196;
0; Mismatches 25;
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                        Query Match
Best Local S
Matches 535
                                                                                                                     W09743427-A1.
20-N0V-1997; E02443.
13-MAY-1996; GB-010044.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De VI1es SC, Hecht VFG, S
WPI; 98-086529/08.
                                                                                                                                                                                                 Arabidopsis
Key
CDS
                                                                                                                                                                                                                                                    V06589 standard; cDNA to mRNA;
V06589;
03-AUG-1998 (first entry)
                                                                   p-pSDB; W47021.

Production of apomictic seeds - useful in plant bi Claim 28; Pages 83-84; 123pp; English.

The sequence is that of an EST clone showing high SERK LRR (leucine-rich repeat) sequences.

Sequence 894 BP; 270 A; 163 C; 176 G;
                                                                                                                                                                                                                           03-AuG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST receptor kinase; apomixis; apomictic; seeds; plant breeding; leucine-rich repeat; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       545
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ctccgaaggagatgctctctacgctcttcgccggagtttgacagatccagaccatgtcct
                        al Similarity
535; Conser
                                                                                                                                                                                                                                                                                                                                  882
                                                                                                                                                                                                                   thaliana.
                         Conservative
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                                 36.3%;
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                                                                                                                               Schmidt
                       ; Score 356.2; D; Pred. No. 2.2e-
0; Mismatches
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production;
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            W09743427-A1.
20-N0V-1997.
13-MAY-1996; GB-010044.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, $
WPI; 98-086529/08.
                                                                                         03-AUG-1998 (first entry)
Arabidopsis thaliana SERK (
receptor kinase; apomixis;
plant breeding; ds.
                                                                                                                    V06591 standard;
V06591;
      P-PSDB; W47023
                                                                                    Arabidopsis
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Production
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                                                                                                                                                                        caccactttatcaaatatc
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                                                                                     thaliana
apomictic
                                                         /product-
                                                                      Location/Qualifiers
195. .2072
                                                                                                                           CDNA
                                                                 /*tag=
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                   Schmidt
 seeds
                                                                                                                           mRNA;
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                                                                                                 gene.
; apomictic;
                                                           SERK
                                                           protein
                   EDL,
useful
                    Van
                                                                                                  seeds;
in
                     Holst
plant
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RESULT V06571
ID VC
AC VC
DT D;
DE D;
KW T;
KW P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant threeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed apomictic plant sexual plants are available as crosses with the programated hybrids and could shorten and simplify the breeding process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.

Sequence 2089 BP; 568 A; 419 C; 503 G; 599 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
03-AUG-1998 (first entry)
Daucus carota SERK gene.
receptor kinase; apomixis; apomictic; seeds;
plant breeding; ss.
Daucus carota.
                                                                                                  V06571 standard;
V06571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330
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                                                                                                                                                                                                                                             ccctttgctcacattcctttacagaactttgagaacaac 700
                                                                                                                                                                                                                                                                                                  ACCCTTCAAGTGTTAGATCTATCAAATAACAGACTCTCTGGTTCAGTTCCTGACAATGGC
                                                                                                                                                                                                                                                                                                                       agcettaaagttgttgaegteteaageaatgatttgtgtggaacaateecaacaaacgga 661
                                                                                                                                                                                                                                                                                                                                                                              CTCCGGCTTAACAACAACAGTCTCACTGGGTCAATTCCTATGTCACTGACCAATATTACT
                                                                                                                                                                                                                                                                                                                                                                                                     ttacggcttaatgacaaccgattgaccggtccaatccctagagcactcacggcaatccca
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTAAACAGCTTCTCCGGTCCTATTCCGGAATCATTGGGAAAGCTTTCAAAGCTGAGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTCCAGAGCTTGGTGTGCTCAAGAATTTGCAGTATTTGGAGCTTTACAGTAACAACATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACAACGAGAACAGTGTCATAAGAGTTGATTTGGGGGAATGCAGAGTTATCTGGCCATTTA
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                                                                                                                     CDNA; 1814
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Pred. No. 8.1e-49;
0; Mismatches 193
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                                       production;
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                                                   RESULT
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Claim 21; Pages 47-51; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase.
It may be used as part of a method of producing apomictic seeds
comprising: (a) transforming plant material with a nucleotide
sequence encoding a protein which in active form in a cell or
cell membrane renders the cell embryogenic; (b) regenerating
the transformed material into plants or carpel-containing
plant parts; and (c) expressing the sequence in the vicinity
of the embryo sac. The apomictic seeds and embryos thus produced
can be developed into plant progeny. This is useful in plant
breeding programs. Controllable and reproducible apomixis provides
many advantages in plant improvement and cultivar development in
the case that sexual plants are available as crosses with the
capemictic plant. Apomixis provides for true-breeding, seed
propagated hybrids and could shorten and simplify the breeding
process so that selfing and progeny testing to produce and/or
stabilise a desirable gene combination could be eliminated.
Apomixis allows plant breeders to develop cultivars with
seed and forage quality and maturity.

Sequence 1814 BP; 530 A; 354 C; 415 G; 515 T;
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 X23526 standard; DNA; 5940 BP. X23526;
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Pred. No. 7.8e
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7.8e-19;
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Best Local Similarity
Matches 165; Conserv
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Oryza longistaminata.
W09909151-A2.
25-FEB-1999; U14841.
17-JUL-1998; U1-910386.
(REGC) UNIV CALLFORNIA.
Hulbert SH, Richter T, Roi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plants. The invention describes the use of novel genes and proteins belonging to the Oryza longistaminata and Oryza sativa receptor kinase-like protein (RRK) Xa21 multigene family. Such genes from cassava, maize and tomato are also described. The genes and proteins can be used for enhancing resistance to Xanthomonas in a plant, preferably in rice or tomato.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New RRK polynucleotides and nucleic acid constructs - used for generating transgenic plants resistant to Xanthomonas Claim 1; Page 52-53; 67pp; English.
This invention describes a method for conferring disease resistance
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O. longistam
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                                                                                                                            03-AUG-1998 (first entry)
Daucus carota SERK gene.
receptor kinase; apomixis;
plant breeding; ds.
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longistaminta xa21 gene family member A2 DNA.

longistaminta xa21 gene family member A2 DNA.

71 receptor kinase-like protein; multigene family; RRK; rice;

8 ant disease resistance; cassava; maize; tomato; Xanthomonas; s
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99-204431/17
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/number= 1
3851. .3979
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                                                                                                                                         production; embryos;
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CI The sequence is that encoding SERK, a purative receptor kinase.

CI The sequence is that encoding SERK, a purative receptor kinase.

CI The sequence is that encoding SERK, a purative receptor kinase.

CI can be used as part of a method of producing aponictic seeds comprising: (a) transforming plant material with a nucleotide contains a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac: The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides can be developed into plant improvement and cultivar development in the case that sexual plants are available as crosses with the propagated hybrids and could shorten and simplify the breeding process so that selfing and proyeny testing to produce and/or stabilise a desirable gene combination could be eliminated.

Apomixis allows plant breeders to develop cultivars with seed and forage quality and maturity.

Seed and forage quality and maturity.

Sequence 6695-BP; 1844 A; 1182 C; 1243 G; 2422 T;
                                                                                                                                                                                    Query Match
Best Local
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De Vries SC, Hecht VFG,
WPI; 98-086529/08.
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Claim 21; Pages 40-46; 123pp; Er
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13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
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CAGTGTTATAAGAGTGTA 1093
                                                      ctgggatccaactcttgttaatccttgtacctggttccatgtcacctgtaaccaagacaa 312
                                                                                                               AGGCGATGCATTACACAACTTACGAACTAGCTTGCAAGATCCCCAACAATGTCCTGCAGAG
                         ccgcgtcactcgtgtgga
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nilarity 71.0%;
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5295..5803
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Pred. No. 6.6e-
0; Mismatches
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RESULT T62124

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T62124 standard; T62124; 10-JUN-1997 (fir

CDNA

Arabidopsis Key cds

thaliana

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V06585 standard; DNA; 4081 B
V06585;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK ge:
receptor kinase; apomixis; a
plant breeding; ds.
Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; pages 6-10; 17pp; Japanese.
The present sequence encodes an Arabidopsis thaliana plant morphogenesis requiatory protein (MRP), which can be used to yield a plant with, e.g. short stems or altered inflorescence. The MRP acts on a plant at a specific site for a specific period, and can therefore be used to regulate extraneous gene expression in a plant. The MRP's cDNA or genomic DNA can be used to transform a plant to increase its MRP expression, and therefore control the form (particularly stem length) of the plant.

Sequence 3176 BP; 927 A; 654 C; 659 G; 936 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding plant morphogenesis regulatory protein - vield plants with short stems or altered inflorescence Claim 1; Pages 6-10; 17pp; Japanese.
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04-MAR-1997.
24-AUG-1995. 216187.
24-AUG-1995. JP-216187.
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Arabidopsis thaliana plant morphogenesis regulatory protein cDNA.
Plant; morphogenesis; regulation; short; stem; alteration;
inflorescence; extraneous; gene; expression; transformation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            increase; control; form; length;
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                                                                                                                                                                                                                                                                                                                                                                                                                         GTGGCACTATACCCCGGAGCATTTCAAAAGCTAGAAAGTATGACTTACCTTAATCTGTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atttacagtatctagagctctacaaaaacaacatccaaggaactataccttccgaacttg 446
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                                                                                                                                                                                                                                                                                                                      GCAACAATATCAAAGGTCCAATCCC
                                                                                                                                                                                                                                                                                                                                                     gcaatgatttgtgtggaacaatccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGATCATCTGAGCTCTTGCACAAATCTAAACAGCTTAAAATGTTCATGGGAACAAGTTTA
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/note= "plant morphogenesis regulatory protein"
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Location/Qualifiers
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51.7%;
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                                                                                                     gene
                                                                                                                                                                                    ΒP
                                                                            apomictic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 73.8; DF Pred, No. 5.5e: 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                            seeds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
.5e-11;
                                                                            production; embryos;
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                                                                                                     밁
                                                                                                                                                                                                                                                                                                                           Production of apomictic seeds - useful in plant breeding Production of apomictic seeds. CC Claim 26; Pages 64-67; 123pp; English.

CC The sequence is that encoding SERK, a putative receptor kinase. CC It may be used as part of a method of producing apomictic seeds cc comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.

Sequence 4081 BP; 1120 A; 770 C; 785 G; 1406 T;
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                       Query Match
Best Local :
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WPI; 98-086529/08.
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                               ctgggatccaactcttgttaatccttgtacctggttccatgtcacctgtaaccaagacaa 312
                                                                                                     AGGTGATGCTTTGCATACTTTGAGGGTTACTCTAGTTGATCCAAACAATGTCTTGCAGAG
                                                                                                                                                                                                           l Similarity
97; Conserv
                                                                                                                                                                                                           Conservative
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6197. .6339
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/number= 1

3851. .3979

/*tag= c
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/number= 5
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/*tag= e
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/*tag= 1
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/number= 6
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                                                                                                                                                                                                                                 7.4%;
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                                                                                                                                                                                                     Score 72.4; DB 1;
Pred. No. 1.5e-10;
0; Mismatches 41
                                                                                                                                                                                                                                                        Length 4081;
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                           0;
                                                                                                                                                                                                           Gaps
                                                                                                  1853
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Matches

168;

Conservative

985

1105

447

1045

1165

Query Match Best Local Similarity

RESULT
V06585
ID V00
AC V00
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T06307
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Best Local S
Matches 163
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Oryza sativa.
WO9909151-A2.
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New RRK polynucleotides and nucleic acid of generating transgenic plants resistant to Claim 1; Page 48-50; 67pp; English.

This invention describes a method for confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of the confinence of 
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WPI; 99-204431/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plants. The invention describes the use of novel genes and proteins belonging to the Oryza longistaminata and oryza sativa receptor kinase-like protein (RRK) Xa21 multigene family. Such genes from cassava, maize and tomato are also described. The genes and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUL-1998; U14841.
13-AUG-1997; US-910386.
(REGC ) UNIV CALIFORNIA.
Hulbert SH, Richter T, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be used for enhancing resistance to Xanthomonas in a plant, preferably rice or tomato.
14-APR-1996 (first entry)
Partial tomato pathogen resistance
Pathogen resisitant; Cf-2.2; tomato
                                                                                                                                                                                                              3380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3200
                                                                                                T06307 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 tcaaacctctctggacatcttgcgcctgagcttgggaagcttgaacatttacagtatcta 400
                                                                                                                                                                                                                                                         641
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Sativa Xa21 gene family member E DNA.
Sativa Xa21 gene family member E DNA.
Si receptor kinase-like protein; multigene family;
Si receptor kinase-like protein; maize; tomato; Xant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGTGTCATAAGAGTGTA 1931
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                                                                                                                                                                                                                                                         ggaacaatcccaaca
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                                                                                                                                                                                                                                                                                                       TCATCTCTGGGCAAACTCACAGGTCTCACTGATCTTGCACTGGCTGAAAATACGCTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                AATCTAACCAGTCTCGGGTTCTTGAGCTGACTAACAATACACTGTCCGGAGCAATCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
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e 9424 BP;
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                                                                                                cDNA; 3573
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                                                                                                                                                                                                                                                         655
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Matches 147; Conserv
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23-NOV-1995.
11-MAY-1995; G01075.
11-MAY-1994; GB-009394.
13-DEC-1994; W0-G02812.
31-MAR-1995; GB-006658.
07-APR-1995; GB-007232.
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Claim 9; Page 85-87; 131pp; English.

T06307 is a tomato pathogen resistance gene Cf-2.2 partial cDNA clone. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagules of plants) containing such constructs. Cf-2.2 imparts resistance to the disease caused by the leaf mould fungal pathogen Cladosporium fulvum. C. fulvum contains avirulence (Avr) genes that confer recognition by plants containing Cf-genes, leading to the activation of host defence mechanisms to attack the disease.

Sequence 3573 BP; 1032 A; 654 C; 664 G; 1223 T;
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WPI; 96-010949/01.
P-PSDB; R85299.
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23-NOV-1995.
11-MAY-1995; G01075.
11-MAY-1994; GB-009394.
23-DEC-1994; WO-G02812.
33-MAR-1995; GB-007658.
07-APR-1995; GB-007232.
(GATS-) GATSBY CHARITABLE FV Hammond-Kosack KE, Jones D. WPI; 96-010999/01.
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706306 is the tomato pathogen resistance gene Cf-2.1. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagules of plants) containing such constructs. Cf-2.1 imparts resistance to the disease caused by the leaf mould fungal pathogen Cladosporium fulrum. C.fulrum contains avirulence (Avr) genes that confer recognition by plants containing Cf-genes, leading to the activation of host defence mechanisms to attack the disease.

Sequence 6471 Bp; 2073 A; 1106 C; 1122 G; 2170 T;
p-PSDB; w93596.

New RRK polynucleotides and nucleic acid constructs - generating transgenic plants resistant to Xanthomonas Claim 1; Page 37-39; 67pp; English.
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13-AUG-1997; US-910386.
(REGC ) UNIV CALIFORNIA.
Hulbert SH, Richter T, R
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Oryza longistaminata.
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WO9909151-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   belonging to the Oryza longistaminata and Oryza sativa receptor kinase-like protein (RRK) Ka21 multigene family. Such genes from cassava, maize and tomato a laso described. The genes and proteins cabe used for enhancing resistance to Kanthomonas in a plant, preferably rice or tomato.
                                                       5266
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                                                                          agagcactcacggcaatcccaagccttaaagttgttgacgtctcaagcaatgatttgtgt
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Search completed: June 23, 2000, 22:53:01 Job time: 40577 sec

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Title:
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1: /cgn2_6/ptodata/
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3: /cgn2_6/ptodata/
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PATENT NO. 5952445
GENERAL INFORMATION:
GAPPLICANT: ROTALD:
APPLICANT: ROTALD:
APPLICANT: Wang, Guo-Liang
APPLICANT: Scabo, Veronique
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: PATENTION EPO-DOS/MS-DOS
SOFTWARE: DATE: 04-DEC-195
CLASSIFICATION NUMBER: US/08/567,375
FILING DATE: 04-DEC-195
CLASSIFICATION NUMBER: US/08/567,375
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US/08/567,375
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US/08/767,375
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US/08/767,375
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US/08/767,375
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US/08/767,375
FILING DATE: 17-JAN-199
APPLICATION NUMBER: US/08/373,375
FILING DATE: 07-JUN-1995
ATTORNEY/ACENT INFORMATION:
NAME: Bastian, Kevin L
REGISTRATION NUMBER: US/08/373,375
FILING DATE: 17-JAN-199
APPLICATION NUMBER: US/08/373,375
FILING DATE: 07-JUN-1995
ATTORNEY-ACENT INFORMATION:
NAME: Bastian, Kevin L
REGISTRATION NUMBER: US/08/373,375
FILING DATE: 17-JAN-199
APPLICATION NUMBER: US/08/373,375
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APPLICATION NUMBER: US/08/373,375
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SEQUENCE CHARACTERISTICS:
LEUGH: 3921 base pairs
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Best Local Similarity 49.9
Matches 169; Conservative
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                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,680A
FILING DATE: 17-JAN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
FILING DATE: 17-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1459 CCAATACCCAGTGAATTATTCAATATTCAAACACTATCA 1497
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                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            524
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LOCATION: join(1.
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two Embarcadero CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTACTGAACTTAATATCTTACTGCTCGGCACCAACAATTCAGTGGTTGGATACCATAC 1398
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APPLICATION DATA:
LICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang, Guo-Liang
Song, Wen-Yuang
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www.sarion: /product= "xa-21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Townsend and Townsend and Crew LLP TOWNSEND AND TOWNSEND TO EMBARCAGETO Center, Eighth Floor
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                                                               US 08/475,891
US 60/004,645
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Pred. No. 4.7e-10;
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; NAME/KEY: CDS
; LOCATION: Join(1..2676, 3520..3918)
; OTHER INFORMATION: /product= "Xa-21"
US-08-587-680A-3
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3921 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08475891A Patent No. 5859339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 169;
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Best Local
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
                                                                                          APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
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Local Similarity 49.9%;
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                                     COUNTRY:
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                   94111-3834
                                                                               San Francisco
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READABLE FORM
                                                           California
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NAME/KEY: CDS
| LOCATION: Join(512.
| OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION:
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US-08-238-163-3
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5992 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                      Sequence 3, Application US/08238163 Patent No. 5569830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                 GENERAL INFORMATION:
APPLICANT: BENNET'
APPLICANT: LABAVI'
APPLICANT: POWELL
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APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
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TELEFAX: (415) 576-0300
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REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: II
                                                                                                                                                                                                                       acaatcccaacaggaccctttgctcacattccttta 682
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                                                                                                                                                                                                                                                                     ACACTCTCAAAACCTCACAAACTTGTTGTCATTAGGCCCTTTCAACTAATAACCTTAGTGGT 1969
                                                                                                                                                                                                                                                                                                      gcactcacggcaatcccaagccttaaagttgttgacgtctcaagcaatgatttgtgtgga 643
                                                                                                                                                                                                                                                                                                                                                                CCAATACCCAGTGAATTATTCAATATTCAAACACTATCA 2008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                BENNETT, Alan
LABAVITCH, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
POWELL, Ann
STOTZ, Henrik
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RMATION: /product= "RK-B"

RMATION: /product= "RX-B from rice (Oryza
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Pred. No. 5.8e-10;
0; Mismatches 170;
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; NAME/KEY: ; LOCATION: US-08-238-163-3
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Best Local Similarity 49.0%;
Matches 221; Conservative
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COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/00
FILING DATE: 03-MAY-1994
CLLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
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FEATURE:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   621 tctcaagcaatgatttgtgtggaacaatccc 651
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                                                                                                                                                                                                                               441 aacttggaaatctgaagaatctcatcagcttggatctgtacaacaacaatcttacaggga 500
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REGISTRATION NUMBER:
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                                                                                                                              CGATCCCTGAATTCCTTAGTCAGCTGAAGAATTTGACGTTGCTCGAGTTGAATTACAATC
                                                                                                                                                      tagttcccacttctttgggaaaattgaagtctctggtctttttacggcttaatgacaacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTACAAATAAAGAAAGACTTAGGCAATCCTTACCATTTAGCTTCATGGGATCCAAACAC 572
                                                                                      gattgaccggtccaatccctagagcactcacggcaatcccaagccttaaagttgttgacg 620
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Pred. No. 3.3e-08;
0; Mismatches 223;
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TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
TYPE: nucleic acid
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Patent No.
                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 168; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Guo-Liang APPLICANT: Song, Wen-Yuang
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
2855
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                                                                                                                                                  2735 TGGACTTGGGAGAAAATAACCTGGGGGGGAGTTCTTCCTAATTCGTTTTCCAATCTTTCCA 2794
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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STATE: California
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REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/373,375 FILING DATE: 17-JAN-1995
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FILING DATE: 06-JUN-1995
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LOCATION: joir
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                    ttggaaatctgaagaatctcatcagcttggatctgtacaacaacaatcttacagggatag 503
                                                                                              att---tacagtatotagagototacaaaaacaacatocaaggaactatacottocgaac 443
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                                                                          CTTCGCTTAGTTTTCTTGCACTTGATTTGAATAAGATCACAGGAAGCATTCCAAAGGATA 2854
TTGGCAATCTTATTGGCTTACAACATCTCTATCTCTGCAACAACAATTTCAGAGGGTCAC 2914
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                                                                                                                                                                                                                                             6.1%;
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/note= "xa21 xanthomonas spp. disease
resistance gene RRK-F from rice (Oryza
sativa)"
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Pred. No. 5.6e-08;
0; Mismatches 158;
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US-08-567-375-1
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APPLICATION NUMBER: US 08/475,891

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/373,375

FILING DATE: 17-JAN-1995

ATTORNEY/AGENT INFORMATION:
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APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
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                                                                                                                                        FEATURE:
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CITY: San Francisco
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                                                                          LOCATION: join(16.
OTHER INFORMATION:
                                                                                                                                                                                            LENGTH: 6256 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                     INFORMATION: INFORMATION:
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Song, Wen-Yuang
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                                                                                                                                                                                  linear
                                                       join(1648..4383, 5178..5513)
WATION: /product= "RRK-F"
WATION: /note= "Xa21 Xanthomonas spp. disease
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                                                                                                                                                         DNA (genomic)
                  resistance gene RRK-F from (Oryza sativa)"
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US-08-587-680A-1
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP
ADDRESSEE: Townsend and Townsend and Crew LLP
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                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/00 FILING DATE: 17-JAN-1996 CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                             APPLICATION NUMBER: US 08/567,375 FILING DATE: 04-DEC-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2795 CTTCGCTTAGTTTTCTTGCACTTGATTTGAATAAGATCACAGGAAGCATTCCAAAGGATA 2854
                                                                                            APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
FRIOR APPLICATION DATA:
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Local Similarity 51.1%;
hes 168; Conservative
                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/373,375 FILING DATE: 17-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
NAME: Bastian, Kevi
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           att---tacagtatctagagctctacaaaaacaaccatccaaggaactataccttccgaac 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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Song, Wen-Yuang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ronald, Pamela C.
                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
34,774
                                                                                                                                                                                                                                                                                                                                     US/08/587,680A
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Pred. No. 5.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 158;
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RESULT 8
US-08-238-163-1
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                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: BENNETT
APPLICANT: LABAVII
APPLICANT: POWELL,
APPLICANT: STOTZ,
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08238163 Patent No. 5569830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
TYPE: nucleic acid
          LIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 023070-058940US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
TELEPAX: (415) 576-0300
TELEPAX: (415) 576-0300
TELEPAX: (415) 576-0300
                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STEET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2975
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                                                                                                                                                                                                                                         TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3035 GCACCAACAAATTCAGTGGTTGGATACCA 3063
                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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LOCATION: join(1648...4383, 5178...5513)
OTHER INFORMATION: /product= "RRK-F"
OTHER INFORMATION: /note= "xa21 xantho
OTHER INFORMATION: resistance gene RRK
OTHER INFORMATION: sativa)"
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                                                                                                COUNTRY:
                                                                                                                                           CITY:
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  OPERATING SYSTEM:
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                                                                                                                                           San Francisco
                                                                                                                     California
                                                                                                                                                                                                                                                                                                                                         BENNETT, Alan
                                                                                                                                                                                                                                                                                                                      LABAVITCH, John
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STOTZ, Henrik
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compatible
PC-DOS/MS-DOS
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/notc= "xa21 Xanthomonas spp. disease
resistance gene RRK-F from rice (Oryza
sativa)"
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Pred. No. 5.6e-08;
0; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 6256;
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; LOCATION: 1..1058
; OTHER INFORMATION: /standard_name= "Pear PGIP cDNA"
US-08-238-163-1
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US-08-473-553A-1
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NAME: BASTLAN, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                    Sequence 1, Application US/08473553A Patent No. 5859338 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.8%;
Best Local Similarity 52.0%;
Matches 127; Conservative
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NAME/KEY: misc_feature

*OCATION: 1..1058
                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach,
STREET: Four Embarcadero C
                                                                                                                                     APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 caaacctctctggacatcttgcgcctgagcttgggaagcttgaacatttacagtatctag 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347 CCAATCTCACTGGCCCAATCCAACCCGCCATTGCCAAGCTCAAAGGACTCAAGTCTCTCA 406
                                                                                                                                                                                                                                                                                                                                                                                      587 TATC 590
                                                                                                                                                                                                                                                                                                                                                                                                                       582 gagc 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                           527 AGCTCCCAAACCTCGGCGCTCTTCGTCTAGACCGCAATAAGCTCACAGGTCATATTCCGA 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0
FILING DATE: 03-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tcatcagcttggatctgtacaacaacatcttacagggatagttcccacttctttgggaa 521
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             94111-4187
                                                                     San Francisco
                                                      California
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34..1023
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Center,
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Pred. No. 2.3e-07;
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                                                                                      Albritton & Herbert
Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117;
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US-08-587-680A-24
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CLASSIFICATION: 800
ATTORNEY APPLICATION BORDER: US/08/473,553A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
ATTORNEY/Account
                                                                                                                                                                                                                                   Sequence 24, Application US/08587680A Patent No. 5977434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.6%;
Best Local Similarity 51.0%;
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 5733 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLE
STREET: Two Embarcadero Center, Eighth Floor
                                                                      APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                        3360 AATCCCTCAAAGC 3372
                                                                                                                                                                                                                                                                                                                                                                                                                                    3240 GAAACATCTACATACTCTGTTTCTTCACATCAACAACTTAACCGGTCATATACCACCGGA 3299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3120 CTACTACAACAGCTACACCGGTGGTGTTCCACGCGAGTTCGGTGGTTTAACAAAGCTTGA 3179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            406 ctacaaaaacaacatccaaggaactataccttccgaacttggaaatctgaagaatctcat 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     526 gaagtetetggtetttttaeggettaatgaeegattgaeeggteeaateeetagage 585
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                                                                                                                                                                                                                                                                                                                                                                                             646 aatcccaacaaac 658
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San Francisco
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2434..5037
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Pred. No. 2.3e-06;
0; Mismatches 124;
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COMPUTER READABLE FORM:

COUNTRY:

STATE: California

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                                                                                                                                                                                    US-08-567-375-15
Sequence 15, Application:
Sequence 15, Application:
Patent No. 5952485
GENERAL INFORMATION:
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FILING DATE: 04-DEC-127.

ATTORREY/AGENT INFORMATION:

NAME: Bastian, Kevin L.

REGISTRATION NUMBER: 34,774

REFERENCE/DOCKET NUMBER: 023070-058940US

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 1.576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.5%;
Best Local Similarity 49.1%;
Matches 143; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 29-SEP-1995
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ON NUMBER: US 08/373,375
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COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cagcttggatctgtacaacaaccaatcttacagggatagttcccacttctttgggaaaatt 525
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                                                                                                                                                                                                                                                                                                                                                                                                    actcacggcaatcccaagccttaaagttgttgacgtctcaagcaatgattt 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTTTCCTTAACTTACTTGGATTTGAGCCAAAATCAACTTTCTGGTCCTATCCCAGTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTGTCTGGTGCACTTCCTAGTGCTATTGGAAACTATTCAGGGCTGAAGAATCTTGTGTT 77
                                                                                                                                                                                                                                                                                                                                          AATTGCTCAAATTCACATCTTAAATTACATCAATATTTCCTGGAATCACTT 308
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DEDNESS: single
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04-DEC-1995
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Pred. No. 1.6e-06;
0; Mismatches 148;
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; TOPOLOGY: 11; MOLECULE TYPE: US-08-567-375-15
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ETILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/ACENT INFORMATION:
NAME: SECTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,375
FILING DATE: 04-DEC-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Procedures and Trible OF INVENTION: Disease Resistance in Plants of SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)_576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 831 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                             153
                                                                                                                                                                                                                                                                    411 aaaacaacatccaaggaactataccttccgaacttggaaatctgaagaatctcatcagct 470
                                                                              213
                                                                                                    531 ctctggtctttttacggcttaatgacaaccgattgaccggtccaatccctagagcactca 590
                                                                                                                                                                                                     471
273 CTCAAATTCACATCTTAAATTACATCAATATTTCCTGGAATCACTT
                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 138; Conserv
                                                                                                                                                                                                                                            93 GANATGGTTTCTCAGGTGATATCCCTTCTGATATTGGCAGACTAAAGAGCATCTTAAAGC 152
                                                                                                                                                                                                                                                                                                                             33 CTGGTGCACTTCCTAGTGCTTTTGGAAACTATTCAGGGCTGAAGAATCTTGTGTTAACTG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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                                   cggcaatcccaagccttaaagttgttgacgtctcaagcaatgattt 636
                                                                            CCTTAACTTACTTGGATTTGAGCCAAAATCAACTTTCTGGTCCTATCCCAGTTCAAATTG
                                                                                                                                                             TGGACTCGAGTAGAAACAACTTCTCTGGCACAATCCCTCCTCAGATTGGTAACTGTCTTT
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Szabo, Veronique
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48.3%;
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Pred. No. 3.3e-05;
0; Mismatches 148;
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318
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                                                                                                                                                                                                                                                                                   Query Match 4.9%;
Best Local Similarity 48.5%;
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE: 24-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 940
FILING DATE: 11-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 622
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/02812
FILING DATE: 23-DEC-1994
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                                                                                                                                          2133
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                                                                                                                                                                                                                2073 TATCAATCTCTCAAAGAACAGATTTGAAGGTCATATTCCAAGCATTATTGGAGATCTTGT 2132
                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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PRIOR APPLICATION DATA:
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                  577 ccctagagcactcacggcaatccccaagccttaaagttgttgacgtctcaagcaattgattt 636
                                                                                                                                                                            457
                                                                                                                                                                                                                                    397 tctagagctctacaaaaccaacatccaaggaactataccttccgaacttggaaatctgaa 456
                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2880 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                               gggaaaattgaagtetetggtetttttacggettaatgacaaccgattgaccggtecaat 576
TGGACTTCGTACGTTGAACTTGTCTCACAATGTCTTGGAAGGTCATATACCGGCATCATT 2192
                                                                                                                                                                        gaatctcatcagcttggatctgtacaacaacaatcttacagggatagttcccacttcttt 516
                                                                   TCAAAATTTATCAGTACTCGAATCTTTGGATCTCTCATCTAATAAAATCAGCGGAGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
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THOMAS, COLWYN M
JONES, DAVID A
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                                                                                                                                                                                                                                                                                                                                                                                                               linear
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11-MAY-1994
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M-KOSACK, KIM E
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                                                                                                                                                                                                                                                                                                    Score 48.4; DB 4
Pred. No. 0.0001;
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                                                                                                                                                                                                                                                                                                                   DB 4;
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2312
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; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-666-271-1
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Query Match
Best Local Similarity 48.5
Matches 133; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 62
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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LENGTH: 3905 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 11-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                          NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: GB 9 FILING DATE: 24-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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1100 NORTH GLEBE ROAD, 8TH FLOOR
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THOMAS, COLWYN M
JONES, DAVID A
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898..3489
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898..966
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967..3486
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D-KOSACK, KIM E
                48.5%;
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Score 48.4; DB 4;
Pred. No. 0.00012;
0; Mismatches 141
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   141;
                              Length 3905;
   Indels
   0;
   Gaps
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397 tctagagctctacaaaaacaacatccaaggaactataccttccgaacttggaaatctgaa 456

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US-08-232-463-14
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US-08-232-463-14
        Best Loc
Matches
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                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/07/935
APPLICATION NUMBER: US/07/935
FILING DATE:
APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY_AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3093
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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  y Match 4.8%; Score 47.4; DB 1; Local Similarity 3.5%; Pred. No. 0.00032; hes 12; Conservative 194; Mismatches 135;
                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
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                                                                                                                                                                                                              SS: single
linear
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                                                    Length 7218;
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US-08-244-646-14
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Patent No. 5
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
SEQUENCE 1116 base pairs
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APPLICANT: Cervon
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APPLICATION NUMBER: IT RM
FILING DATE: 06-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: SUILLYAN, SALLY A.
REGISTRATION NUMBER: 32,06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compa
OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Sally A. Sullivan STREET: 5370 Manhattan Circle Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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Salvi, Giovanni
Albersheim, Peter
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SYSTEM: PC-DOS/MS-DOS
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06-JUN-1994
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Search completed: June 23, 2000, 22:45:22 Job time: 40268 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phaseolus vulgaris
STRAIN: Saxa
IMMEDIATE SOURCE:
CLONE: lambda PGIP-3.3
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Perfect score:
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Listing first 45
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Maximum DB seq length: 1000000
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     June 23, 2000, 19:06:32; Search time 6198.48 Seconds (without alignments) 641.482 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

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AI992868 469 bp mRNA EST 08-SEP-1999 N 701493826 A. thaliana, Ohio State clone set Arabidopsis thaliana cDNA clone 701493826, mRNA sequence. AI992868 AI992868.1 GI:5839773 EST. thale cress. Arabidopsis thaliana Estarbidopsis thaliana Arabidopsis thaliana Estaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases I to 469) 1 (bases I to 469) Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and	ALIGNMENTS	23.6 515 79 AW279515 23.6 612 47 AI496325 23.5 541 64 AW036865 23.4 619 64 AW040482 23.2 304 36 T21150 22.9 568 47 AI487272 22.8 423 35 C22371 22.8 423 35 C22371 22.6 570 50 AI676939 22.0 540 64 AW037599 21.9 258 42 AI100678	27.3 599 27.2 3059 27.2 3059 26.6 637 26.1 637 25.9 442 25.9 442 25.8 430 25.8 536 25.9 456 25.9 529 24.6 536 546 557		Match Length DB ID 41.1 469 63 AI992868 39.2 556 23 R89998 36.7 534 33 AA394359 36.0 447 23 H36800 35.0 401 37 AA712221 34.2 353 23 H37300 33.9 364 42 AI100683 33.9 364 42 AI100683
Oy 417 acatccaaggaactataccttcgaaatctgaagaatctcatcaggcttggatc 476	atottgogoctgagottgggaagottgaacatttacagtatctagagottotacaaaacat 	163 TCGAAGCAAACTCCGAGGAGGAGGTCTTTACGCTCTTCGCCGGAGTTTAACAGATCCGG 237 accatgtcctccagagctgggatccaactcttgttaatccttgttacctggttccatgtca [Query Match Query Match Best Local Similarity 96.5%; Pred. No. 8.6e-92; Matches 412; Conservative 0; Mismatches 15; Indels 0; Gaps 0; Qy 57 ctcaaattccttttcgatttccctctcttaaacctccgaaagctcacatggcgtctcgaa 116	omesystems.com. Qualifiers "unabidopsis thaliana" "taxon:3702" 01493826" b="A. thaliana, Ohio State clor bb="A. thaliana Ohio State clor NA library was made from select is thaliana Ohio State clone s 18 g g 136 t	H 700 t F0;

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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                                               ttgg-agggaccggaattactcggtcttgcaagctacgacactaactgcacctgaaacaa 765
                                                                                                                                                                                                                  AAGTCTCTGGTCTTTTTACGGCTTAATGACCAATCGATTGACGGGGCCAATCCCTAGAGCA
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ctggcaaaacctgaaaatgaagaattggggggtgaccttgtaagaac
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                               TTGGNAGGGACCGGAATTACTCGGTCTTGCAAGCTNCGGCAATAACTGACC---TGAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Apr 14, 1993 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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primer: T7 dye primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oligo dT primed cDNA.
118 c 123 g
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/clone_lib="Lambda-PRL2"
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/strain="var columbia"
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Pred. No. 4.9e-87;
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CACTCACGGCAATCCCAAGCCTTAAAGTTGTTGACGTCTCAAGCAATGATTTGTGTGGAA
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1 (bases 1 to 534)

1 (bases 1 to 534)

Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Ketzel, E. and Somerville, C.

Retzel, E. and Somerville, C.

Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones plant Physiol. 106, 1241-1255 (1994)

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euphyllophytes; Spermatophyta; Magnoliophyta;
eudicots; Rosidae; eurosids II; Brassicales;
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Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
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Lambda-PRL2
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114 c 125 g 126 t 18 others
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/db_xref="taxon:3702"
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Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
Michigan State University, Plant Biology
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Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Ralkhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C.
Retzel, E. and Somerville, C.
Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
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Tel: 517-353-0854
Fax: 517-353-9168
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/clone="179A22T7"
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AA712221.1
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31949 Lar
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95148729

On Sep 19, 1997 this sequence version replaced gi:1520373.

Contact: Thomas Newman

MSU-DOE Plant Research Laboratory

Michigan State University

MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
                                                                                                                                                                                                                                                                                                                                         MCIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Industry, Retzel,E. and Somerville,C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA (plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                  Lansing, Mi
Tel: 517-353-0854
Fax: 517-353-9168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
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83; Conservative
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                                                                                                                                           il: 22313tcn@ibm.cl.msu.edu
primer: T7 dye primer.
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Lambda-PRL2
/organism="Arabidopsis th
/strain="var columbia"
/db_xref="taxon:3702"
/clone="18009T"
/clone_lib="Lambda-PRL2"
/note="Vector: lambda Zip
                                                                                                               1. .401
                                                                                                                          Location/Qualifiers
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92.3%;
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Raikhel,N., Somerville,
Zip-Lox;
                                                                                            thaliana'
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   Sal;
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,S., Thomashow, M.,
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   Site_2:
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AUTHORS
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Best Local S
Matches 363
                                                                                                                                    TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363;
                                                                                                                                                                                                                                                                                                 sequence.
H37300
H37300.1 GI:
EST.
thale cress.
                                                                                             Newman,T., deBruijh,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow, Retzel,E. and Somerville,C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA cl Plant Physiol. 106, 1241-1255 (1994)
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15429 1
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
              95148729
On May 8, 1995 this sequence versi
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
                                                                                                                                                                                                                    Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                (bases 1 to 353)
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                                                                                                                                                                                                                                                                                                                                                                                    0 353
Lambda-PRL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA. 78 g 99 t 16 others
 Michigan
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Arabidopsis
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Pred. No. 8.8e-77;
 State
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University, Plant Biology Bldg.,
                                                                   version
                                                                                                                                                                                                                                                                                                                                                                                      thaliana
                                                                 replaced
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179J19T7, mRNA
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ACCESSION
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Best Local S
Matches 337
                                                                                            AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGGAGGGNCCGGANTTACTCGGTCTTGCAAGNTACGGCACTAACTGCANCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttggagggaccggaattactcggtcttgcaagctacgacactaactgcacctg
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Tel: 517-3
Fax: 517-3
Arabidopsis.

1 (bases 1 to 364)

1 (bases 1 to 364)

Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., Newman, T., deBruijn, F.J., Raikhel, N., Somerville, S., Thomas McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomas McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomas McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomas McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomas McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomas McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomas McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomas McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomas McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomas McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomas McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomas McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomas McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomas McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomas McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomas McIntosh, R., Somerville, S., Thomas McIntosh, R., Somerville, S., Thomas McIntosh, R., Somerville, S., Thomas McIntosh, R., Somerville, S., Thomas McIntosh, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerville, R., Somerv
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
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//Clone_lib="Lambda PRL2"
//Clone_"Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
//Indic="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
//Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 h light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA.

98 a 85 c 67 g 89 t 14 others
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/clone="179J19T7"
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/strain="var columbia"
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Tel: 517-353-0854

Fax: 517-353-9168

Email: 22313tcn@ibm.cl.msu.edu

The sequence entry for this EST ha

is being submitted in the sense or

Seq primer: M13-21.
                                                                                                                                                                                             AGCAATGATTTGTGTGGAACAATCCCAACAAACGGACCTTTTGCTCACATTCCTTTACAG
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  Z34187
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//note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
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/strain="var columbia"
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AUTHORS
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AI100682.1 EST.

sequence.

AI100682 348 33803 Lambda-PRL2

bp mRNA
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thaliana

EST cDNA clone

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Query Match
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                  tctgtatgtaaaaatttctaaaatgcgattttcgc 965
                                                                                                acaaaaaaaatgaagaatcgaatcggtaatatcatctggtctcaatttgagaacttcgagg
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TCTGTATGTAAAATTTCTAAAGTCGATTTTCGC
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Route de Saint-Cyr, 78026 Versailles
Email: thierry@versailles.inra.fr.
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/clone_Tib="Versailles-VB"
/tissue_type="whole seedlings"
/dev_stage="in vitro-grown etiolated seedlings,5
/dev_stage="in vitro-grown etiolated seedlings,5
/note="Vector: pBluescript"
/note="Vector: pBluescript" 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Arabidopsis thaliana"
/strain="ecotype Columbia"
/db_xref="taxon:3702"
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Pred. No. 4.8e-73; 
0; Mismatches :
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17-FEB-2000

Bowman, C

Holt, I.E.,

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321;
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                                                                                                                                                                                              CCGGBATTACTCGGTCTTGCAAGCTACGACCTGAACCTGGACACACTGGCAAAAC 775
                                                                                                                                                                                                                                                                               aacggaccctttgctcacattcctttacagaactttgagaacaacccgagattggaggga 715
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                                                                                                                                                                                                                                                                                                                                                                                                                          GTCTTTTTACGGCTTAATGACAACCGATTGACGGGGCCAATCCNTAGAGCACTCACTGCA 73
                          CTGAAAATGAAGAATTGGGGGGGTGANCTTGTAAGAACACTTCACCACTTTATCAAATATC
                                                                                                             ctgaaaatgaagaattggggggtgaccttgtaagaacacttcaccactttatcaaatatc 835
                                                                                                                                                                        CCGGAATTACTCGNTCTTGCAAGCTACGACACTAACTGCACCTGAAAAAATTGGCAAAAC
                                                                                                                                                                                                                                                      AACGGACCTTTTGCTCACATTCCTTTACAGAACTTTGAGAACAACCCGAGGTTGGAGGGA 193
                                                                                                                                                                                                                                                                                                                                       ATCCCAAGCCTTAAAGTTGTTGATGTCTCAAGCAATGATTTGTGTGGAACAATCCCAACA 133
      ACATCTACTATGTAATAAGTATATATGTAGT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On May 5, 1995 this sequence version
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 348)
Newman,T., deBruijn,F.J., Green,P., K.
McIntosh,L., Ohlrogge,J., Raikhel,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E
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Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: 22313tcn@ibm.cl.msu.edu
The sequence entry for this EST
is being submitted in the sense
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/strain="var columbia"
/strain="taxon 3702"
/db_xref="taxon: 3702"
/clone="18511XP"
/clone=lib="Lambda-PRL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inote="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PL2 is a CDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) and a germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and sliques. The vector is BRL's lambda Zip-Lox. The CDNA inserts were directionally cloned with Sal-Not arms using ollgo dd primed cDNA. "
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74 c 66 g
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., Somerville,S., Thomashow,M.,
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                                                                       actcgtgtggatttgggaaattcaaacctctctggacatcttgcgcctgagcttgggaag
                                                                                                                           CCAAATCTTGTTAACCCTTGTACCTGGTTTCATGTCACTTGCAACGGAGATAATCAAGTT
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cttgaacatttacagtatctagagctctacaaaaacaacatccaaggaactataccttcc
                                        ACTCGTGTGCATCTTGGGAACTCAAAGTTATCTGGTCATTTGGTACCTGAGCTCGGAAAG
                                                                                                                                                                                                                                                                                                                                                                                 411;
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100 Jordan Hall, Cl
Tel: 864 656 4366
Fax: 864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST308135 tomato mixed elicitor, clone cLET43M10 5', mRNA sequence AW443205
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Eukaryota; Viridiplanta
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Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Dec 20, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tomato
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Vector: pBlueScript sK(-); Site_1: EcoR1; Site_2: Xhol; CLET - Incoulated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenthion, EIX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="tomato mixed elicitor,
/tlssue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="xil-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Tycopersicon esculentum"
/cultivar="Rio Grande PtoR"
/db_xref="taxon:4081"
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                                                                                                                                                                                                                                                                                                                                                                               Score 312.6; DB 8
Pred. No. 6.2e-69;
0; Mismatches 164
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1 (bases 1 to 720)

Alcala,J., Vrebblov,J., White,R., Matern,A.L., Vision,T., Alcala,J., Vrebblov,J., White,R., Matern,M.B., Bowman,C.L., Holt, T.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
AW031110
AW031110.1 GI:5889866
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100 Jordan Hall, Clemson, SC 29634, U
                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
On Dec 20, 1995 this sequence
Contact: David Frisch
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               ø
                          /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; supplier: Giovannoni laboratory; cLEC - Cotyledons of seedlings 7-10 days post-germinatory excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library"
                                                                                                                                   /clone="CLECI3044

/clone_lib="tomato callus, TAMU"

/tissue_type="callus"

/tissue_type="callus"
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                                                                                                                     /dev_stage="25-40 days old"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                           /cultivar="TA496"
/db_xref="taxon:4081"
                                                                                                                                                                                                                                                     Location/Qualifiers
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ATTS3366 Versailles-VB
                                                                                                               The Arabidopsis thaliana transcribed genome:
Unpublished (1996)
Contact: Desprez T., Amselem J., Chiapello H
                               Laboratoire de Biologie Cellulaire
Route de Saint-Cyr, 78026 Versailles
Email: thierry@versailles.inra.fr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                             Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University,Plant
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AI100679.1
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33800 Lambda-PRL2
                                                                               Lansing, Mi
Tel: 517-353-0854
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Email: 22313tcn@ibm.cl.msu.edu
The sequence entry for this EST
                                                        Fax: 517-353-9168
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                                                                                                                                                                                                                                            May 5, 1995 this sequence version
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/db_xref="taxon:3702"
/clone="MBVDH02"
/clone_lib="Versailles-VB"
/tissue_type="whole seedlings"
/tissue_type="whole seedlings"
/dev_stage="in vitro-grown etiolated seedlings,5 of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia of the columbia o
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Pred. No. 5e-67;
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 TITLE
JOURNAL
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Seg prime
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clone cLEN6M3, mRNA sequence.
AW221939
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.

Generation of ESTs from tomato fruit tissue Unpublished (1999)
                                                                                                                                 Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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1 (bases 1 to 646)
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/organism="Arabidopsis t
/strain="var columbia"
/db_xref="taxon:3702"
/clone="179J11XP"
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Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark-rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
slilques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA.
a 75 c 66 g 89 t 5 others
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Pred. No. 2.6e-65;
0; Mismatches 17
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                                                                                                                                                                                               cgattgaccggtccaatccctagagcactcacggcaatcccaagccttaaagttgttgac 619
                                                                                                                                                                                                                                                                                                                              atagttcccacttctttgggaaaattgaagtctctggtctttttacggcttaatgacaac
                                                                                                                                                                                                                                                                                                                                                                                         GAGCTCGGTAACTTGAAGAGCCTTATTAGTCTGGATCTGTACAACAACAATATTTCGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAAATCTTGTTAACCCTTGTACCTGGTTTCATGTCACTTGCAACGGAGATAATCAAGTT
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                                                     GTCTCGAATAATGATTTGTGTGGAACAATTCCTACTTCTGGTCCATTTGAGCATATT
                                                                                                                                                                                                                                                                               ACAATTCCTACTTCACTTGGAAAACCTGAAAAACCTTGTTTTCTTGCGTCTAAATGATAAC
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Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 Jordan Hall,
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Contact: David
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ntact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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/clone="clEN643"
/clone="tomato fruit red ripe, TAMU"
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                                                                                                                                          Local
AGTCCCTGTACNNNNNTCCACGTCNNNNGCAANCAGGACANNNNNGTCACTCGAGTGNAT 598
                                                                                                                                          Similarity
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RESULT

Conservative

Indels

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Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Coryell, V., Erpelding, J., Raph, C., Shoop, E., Pardinas, J., Liu, L. and Lewin, H. A Functional Genomics Program for Soybean (NSF 9872565)
Unpublished (1999)
On Nov 22, 1999 this sequence version replaced g1:6462107.
Contact: Vodkin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134. For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888)919-3324 or (314) 427-3222 FAX:(888)919-3324 or (314) 427-3324 or contact:clones@genomesystems.com or info@genome ystems.com web site:www.genomesystems.com or info@genome ystems.com web site:www.genomesystems.com
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Fax: (217) 333-4582
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/note-Wector: pBluescript II XR; Site_1: EcoRI; Site_2:
XhoI; Library Gm-r1021 is a sequence-driven, reracked set
of the original library Gm-c1004 which was prepared from
root cDNA, The mRNA was isolated from entire roots of 8
day old 'Williams' seedlings which were propagated on
paper towels with distilled water. Stratagene's CDNA
Synthesis Kit (catalog #200401) was used to synthesize
the cDNA. The Gm-c1004 library was constructed by Dr.
Paul Keim & Virginia H. Coryell, Department of Biology,
Box5640, Northern Arizona University, Flagstaff, Az
86011, email: paul keiménau.edu, virginia.coryell@nau.edu.
The contig analysis to select unique genes was performed
by the laboratory of Ernest Retzel, Computational Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-vodkin@uiuc.edu
                                                                                                                                                                                                                      University of Illinois,
http://www.life.uiuc.edu/biotech/keck.html."
131 c 120 g 191 t 25 others
                                                                                                                                                                                                                                                                                                                      Reracking was performed by Genome Systems, http://www.genomesystems.com, and sequencing Center for Comparative and Functional Genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Centers, University of Minnesota,
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Score 292.8; DB 80;
Pred. No. 6.4e-64;
0; Mismatches 137;
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Search completed: June 23, 2000, 19:06:35 Job time: 27428 sec

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       June 24, 2000, 00:19:09; Search time 12463.9 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0
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789
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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De. V.S., Schmidt, E.D., Van, H.G. and Hecht, V.F. PRODUCTION OF APOMICTIC SEED Patent: WO 9743427-A 20-NOV-1997;

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            ---agagctctacaaaaacaacatccaaggaactataccttccgaacttggaaatctgaa
                                         TGATTATCTGAAAACATTTACATTATCAGTCACACATATAACATTTTGCTTTGAGTCATA
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1 (bases 1 to 894)

1 (bases 1 to 894)

De, V.S., Schmidt, E.D., Van, H.G. and PRODUCTION OF APOMICTIC SEED Patent: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
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/protein_id="CAB42250.1"
/db_xref="GI:4756646"
/translation="GPIQASEGDALHALRRSLSDPDNVVQSWDPTLVNPCTWFHVTCN
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QHHQVTRLDLGNSNLSGHLVPBLGKLEHLQYLYGIITLLPEDYLKTFTLSVTHTTFCF
ESYSELYKNELGGTIFSELGNLKSLISLDLYNNNLTGKIPSSLGKLKSLVFLRLNENR
LTGPIPRELTVISSLKVVDVSGNDLCGTIPVEGPFEHIPMQNFENNLRLEGPELLGLA
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/db_xref="taxon:32644"
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                                                    /Translation="MESSYVPFILLSLILLPNHSLMLASANLEGDALHTLRVTLVDPN
NVLQSWDPTLVWPCTWFHYTCNNENSVIRVDLGALELSGHLVPELGVLKNLQYLELYS
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LINITTIQPIPSNLGALTMUYSLDLY LANDSGPIPESLGKLKSKLÆFLRLNNNSLGGSIPMS
LINITTIQVLDLSNNRLSGSVPDNGSFSLETPISFANNLDLCGPVTSHPCPGSPPSP
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EPDFFIQPPVSTPSGYGITGALTAGGYAAGAALFFAAFALAFALAGATLAVKTKAK
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                                                                                               Erratum:[[published erratum 1997 Mar;10(2):302]] 2 (bases 1 to 936) Hipskind,J.D.
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Pred. No. 4.6e-50;
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                                                                                                             Direct Submission
Submitted (26-JUN-1996) John D. Hipskind, Bot
Pathology, Purdue University, West Lafayette,
                                                                                                                                                                                                                                                                                       Hipskind, J.D., Nicholson, R.L. and Goldsbrough, P.B Isolation of a cDNA encoding a novel leucine-rich Sorghum bicolor inoculated with fungi
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/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone="SLRR"
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1 (bases 1 to 1755)
Schmidt, E. D., Guzzo, F., Toonen, M.A. and de Vrie
A leucine-rich repeat containing receptor-like
plant cells competent to form embryos
Development 124 (10), 2049-2062 (1997)
                                                                                     Daucus carota

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core

eudicots; Asteridae; euasterids II; Apiales; Aplaceae; Daucus.
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093048.1 GI:2224910
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/db_xref="GI:1710124"
/db_xref="GI:1710124"
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UTSLLESKLQENSLSGAIFASLGNIKALQFSRLNDNMLTGTVFSKSFPLSTFGNLTEL
NTDRNNLDGTRTSSGLRVTAIIQDALKTA"
36...77
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/note="leucine-rich repeat-containing extracellular
glycoprotein; contains six N-glycosylation sites
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Schmidt, E.D.L., Guzzo
Direct Submission
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Submitted (12-MAR-1997) Molecular Biology, Ag
Submitted (12-MAR-1997) Molecular Biology, Ag
Eukaryota;
                         Daucus
                                                         carrot.
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VRGTLGYIAPBYLSTGKSSEKTDVFGYGJMLLELITGQRAFDLARLANDDDVMLLDWV
KSLLKEKKLEMLVDPDLENNYIDTEVEQLIQVALLCTGGSPMERPKMSEVVRMLEGDG
LAEKNDEWQKVEVIHQDVELAPHRTSEWILDSTDNLHAFELSGPR*

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/db_xref="GI:2224911"
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Viridiplantae;
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Pred. No. 5.2e-19;
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  Streptophyta; Embryophyta; Tracheophyta;
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1 (bases 1 to 1815)

De, V.S., Schmidt, E.D., Van, H.G. and Hecht, V.F.

PRODUCTION OF AFOMICTIC SEED
Patent: WO 974347-A 20-NOV-1997;

CIBA GEIGY AG (CH)
                                                                                                                                                                                        498
                                                L.esculentum LRP gene.

X95269

X95269.1 GI:1619299

LRP gene; LRR protein.
                                                                                                             LELRPGENE
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                     tomato.
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LAEKWDEWQKVEVIHQDVELAPHRTSEWILDSTDNLHAFELSGPR"
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/db_xref-"taxon:4039"
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Asteridae; Solananae; Solanales; Solanaceae; Solanum; Potatoe
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1 (bases 1 to 4604)
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                                                                                                                                                                                                                                /gene="LRP"
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3000. .3090
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4283. .4355)
/gene="LRP"
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/gene="LRP"
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/gene="LRP"
/number=5
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/gene="LRP"
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758 c
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/number=3
2709. .2927
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/gene="LRP"
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/gene="LRP"
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/gene="LRP"
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/number=2
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/cultivar="VFN8"
/db_xref="taxon:4081"
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   DB 7;
1e-17;
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                Length 4604;
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Submitted (18-JAN-1996) P. Vera, Universidad Politecnica de Valencia, Inst. de Biologia Molecular y Celular de Plantas, Camino de Vera 14, E- 46022 Valencia, SPAIN

2 (bases 1 to 4604)

Tornero, P., Mayda, E., Gomez, M.D., Canas, L., Conejero, V. and Vera, P. Characterization of LRP, a leucine-rich repeat (LRR) protein from tomato plants that is processed during pathogenesis
                             /translation="meavfriqslfiklwgllavvlavavavkgnsegdalvalrrsl
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IPRELTSISSLKVVDVSNNDLCGTIPTSGPFEHIPLNNFEHNPRLEGPELLGLATYDT
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TITLE
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                               Washington), Genscan (Chris Burge,
http://gnomic.stanford.edu/-chris/ENNSCANW.html), and NetPlantGene
(http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html), searches of the
(http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html), searches of the
complete sequence against a peptide database and the Arabidopsis
EST database at TIGR (http://www.tigr.org/tdb/at/at.html).
Annotated genes are named to indicate the level of evidence for
their annotation. Genes with similarity to other proteins are named
after the database hits. Genes without significant peptide
similarity but with EST similarity are named as 'unknown' proteins.
Genes without protein or EST similarity, that are predicted by more
than two gene prediction programs over most of their length are
annotated as 'hypothetical' proteins. Genes encoding tRNAs are
predicted by tRNAscan-SE (Sean Eddy,
http://groups.unstladd.com/seascan-SE (Sean Eddy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtcgaagcaaactccgaaggagatgctctttacgctcttcgccggagtttaacagatccg 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acctgtaaccaagacaaccgcgtcactcgtgtgga 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTAACGTGTTACAGAGCTGGGATCCAAATCTTGTTAACCCTTGTACCTGGTTTCATGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120;
annotated as 'hypotheticai prodicted by tRNAscan-SE (Sean Eddy, predicted by tRNAscan-SE (Sean Eddy/tRNAscan-SE/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATAC009991 101284 bp DNA Arabidopsis thaliana chromosome III BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (08-OCT-1999) The Institute for Genomic Research,
Medical Center Dr., Rockville, MD 20850, USA
On Oct 8, 1999 this sequence version replaced g1:5902413.
Address all correspondence to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 101284)
Lin.X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Haas,B.,
Lin.X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Haas,B.,
Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Barnstead,M
Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
Arabidopsis thaliana chromosome III BAC F9F8 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                  e-mail: xlin@tigr.org
BAC clone F978 is from Arabidopsis chromosome III and is near the
molecular marker g4547.
The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-SEP-1999) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org 3 (bases 1 to 101284)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lin, X. and Kaul, S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete sequence.
                                                                                                                                                                                                                                                                                                                                                                Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rockville, MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xiaoying Lin
                                                                                                                                                                                                                                                                                                                                        from arthur.epm.ornl.gov), Genefinder (Phil Green,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             le cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bases 1 to 101284)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Institute for Genomic Research
Medical Center Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                   Simple repeats are
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identified by repeatmasker (Arian Smit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4506. .4655,4800. .>5013)
/gene="F9F8.1"
3070. .>5013)
                                                                                     /gene="F9F8.2"
5589. .7932
/gene="F9F8.2"
                                                                                                                                                                                                                                                                                          /proteIn_id="AAF01505.1"
/db_xref="G1:6015678"
/translation="MVGPARPQIVLFGSSIVQMSFGHGGWGAILSEVYARKADIILRG
/YGMNSSRALEVDQVFFKDAAYQPSLVIVYFGGNDSWAPHSSGLGPHVPLTEYVDNM
KKIALHLOSLSDFTRIIFLSSPPVDEAKVRQNQSFYLSEVIRRNDLCKTYSDACVELC
QELGLEVVDLFSTFQKADDWKTVCFTDGIHLSAQGSKIVAGEILRVVKEAEWHPSLHW
KSMPTEFADDSFYDLVSADGKQTVNSSEWTYFWEEQWD"
Complement (5513...5597)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="exon predicted by xgrail, 672. .752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       excellent_shadowexon"
355. .594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="exon predicted by xgrail, complement(2090. .2250)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1182...1357)
/note="exon predicted by marginal_shadowexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="exon predicted by xgrail,
complement(347. .408)
                                                                                                                                                           /note-"exon predicted by xgrail, quality excellent_shadowexon" join(5589. .5795,5897. .5929,6013. .6235,7467. .7932)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(3215. .3325,3565. .
4506. .4655,4800. .5013)
/gene="F9F8.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="exon predicted by 1747. .1838
                   /note="similar to nucleic acid binding protein Alfin-1 GB:AAA20093 [Medicago sativa]" join(5696. .5795,5897. .5929,6013. .6235,7264. .7387,
                                                                                                                                                                                                                                                     complement (5527.
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854. .973
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/chromosome="III"
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/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"unknown protein"
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/gene="F9F8.1"
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(13367. .13468)
/note="exon predicted by xgrail, quality marginal"
/note="exon predicted by xgrail, quality marginal"
/note="exon predicted by xgrail, quality marginal"
/note="exon predicted by xgrail, quality marginal"
complement(join(13822. .14179,14261. .14398,14502. .14582,
16676. .14861,14941. .15033,15124. .15190,15272. .15361,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRTYEGYGSRLGVEKGAILDWNDYYYLHFLPLALKDFNKWPSLPSNIREMNDEYGKEL
VKLGGRLMTILSSNLGLRAEQLQEAFGGEDVGACLRVNYYPKCPQPELALGLSPHSDP
GGMTILLPDDQYVGLQVRHGDTWITVNPLRHAFIVNIGDQIQILSNSKYKSVEHRVIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product "putative leucoanthocyanidin dioxygenase"
/protein id-"AAF01507.1"
/db_xref="G1:6016680"
/tanslation="MNNLDEIXIESKTCLNDQEQEVXIDNMHMSDQDKNKIEIKNKSG
LGEKWPEPIVRVQSLAESNLTSLPDRYIKPPSORPQTTIIDHQPEVADINIPIIDLDS
LFSGNEDDKKRISEACREWGFFQVINHGVKPELMDAARETWKSEFNLPVEAKEVYSNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"similar to leucoanthocyanidin dioxygenase
GB:BAA20143 [Perilla frutescens]"
complement(join(9426. .9674,10198. .10528,11098. .11345,
11491. .11865))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(<9426. .9674,10198. .10528,11098. .11345,
11491. .>11865))
/gene="r9r8.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSIDGQTKSSTPKLMEESYEEEEEEEDEHGDTLCGSCGGHYTNEEFWICCDVCERWYHG
KCVKITPAKAESIKQYKCPPCCAKKGRQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="maaaavssnpriveeifkdysarraallralikdyddfysocdp
EKENICLYGHPNESWEVNLPAEEVPPELPEPALGINFARDGMORKDWLSLVAVHSDCW
LLSVSFYFGARLNRNERKRLFSLINDLPTLFDYVTGRKAMKDNKPSSDSGKKRNKTK
                                                            /protein_id="AAF01508.1"
/db_xref="G1:6016681"
/db_xref="G1:6016681"
/translation="MANIVILEGCIRPLPRIYTTPRSNFLSNNNKFRPSLSSSSYKTS
/translation="MANIVILEGCIRPLPRIYTTPRSNFLSNNNKFRPSLSSSSYKTS
SSPLSFGLNSRDGFTRNMALNVSTPLTTPIFEESPLEEDNKQRPDPGAPPPFNLADIR
AAIPKHCWVKNPWKSLSYVVRDVAIVFALAAGAAYLNNWIVWPLYWLAQCTMFWALFV
LGHDCGHGSFSNDPKLNSVVGHLLHSSILVPYHGWRISHRTHHQNHGHVENDESWHPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      marginal_shadowexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(7717. .7760)
/rpt_family="(CAT)n"
complement(7810. .7847)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative nucleic acid binding /protein_id="AAF01506.1" /db_xref="GI:6016679"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7467. .7727)
/gene="F9F8.2"
                                                                                                                                                                                                /product="omega-3 fatty acid desaturase, chloroplast
precursor"
                                                                                                                                                                                                                                                                                                          complement(join(13988. .14179,14261. .14398,14502. .14582, 14576. .14861,14941. .15033,15124. .15190,15272. .15361,
                                                                                                                                                                                                                                                                                                                                                                           /note="Identical to omega-3 fatty acid desaturase, chloroplast precursor GB:P46310 [Chloroplast Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(13822. .16380)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSEKERVSLAFFYNPKSDIPIQPMQQLVTSTMPPLYPPMTFDQYRLFIRTQGPRGKSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="F9F8.3"
/codon_start=1
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                                        SEKTYNTLDKPTRFFRF¶LPLVMLAYPFYLWARSPGKKGSHYHPDSDLFLPKERKDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="exon predicted by xgrail,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family-"(GA)n"
12824. .12836
                                                                                                                                                                                                                                                                   15662. .16155))
/gene="F9F8.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="F9F8.4
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Best Local Similarity 54.9%;
Matches 167; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44756 CGAGGTTGTCTGCTTTATTACTTTCCCACAATCAGTTCACAGGCACGATTCCTAATAACA 44697
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Submitted (10-JUL-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Chen, S., Harman, P., Hicks, R., Huerta, M., Mason, S., Siepel, J., Zimmerman, M., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Tortumi, M., Yysotskaia, V.S., Walker, M., Yu, G., Ecker, J., Theologis, A. and
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Direct Submission
Submitted (15-JUL-1999) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 943
                                                                                                                                                  Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Chen, S., Harman, P., Hicks, R., Huerta, M., Mason, S., Siepel, J., Zimmerman, M., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
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); Mismatches 137;
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Submitted (18-SEP-1999) DNA Sequencing and Technology Center, Submitted (18-SEP-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 (bases 1 to 116944)

Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Brooks, S., Buehler, E., Chao, O., Dunn, P., Gonzalez, A., Khan, S., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriuni, M., Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and Davis, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  음
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jul 15,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="F3N23.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(1333. .2271,2355. .2966))
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6030. .7079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YKGFHMCKELGLVDRIPRLVCAQAANANPLYLHYKSGFKEDFNPLKANTIFASAIQIG
DPVSIDRAVYALKKSNGIVEEATEEELMDATALADSTGMFICPHTGVALTALMKLRKS
GVIGANDRTVVVSTAHGLKFTQSKIDYHSKNIKEMACRLANPPVKVKAKFGSVMDVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1333. .2966)
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                                                                                                                                                                                                                                                                                                                                                                               complement(join(8272. .86 9161. .9252,9364. .9661))
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complement(8272. .9661)
/gene="F3N23.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ĹYPAVLMKTROOVCHSOGSCIKTAFŤÍ VRHEGLRGLYRGFGTSLMGTIPARALYMTAL
EVTKSSKAVSLGLTEAKAAAVANAYGGLSAAMAAQLVWT PUDVYSORLMVQGSAG
LVNASRCNYVNGFDAFRK TVRADGFKGLYRGFGISILTY AFSNAVMHASVSVADARW
GGIGCYVCKKDEESGNNSTTMKPDSKTIMAVOGVSAAIAGSVSALITMPLDTIKTRLQ
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/db_xref="taxon:3702"
/chromosome="I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , 1999 this sequence version replaced gi:5441915.
Location/Qualifiers
MYSMI PGRVPLPAELTETDPVFVNAKQYHA IMRRRQQRAKLEAQNKLI RARKPYLHES
RHVHALKRPRGSGGRPLNTKKLLQESEQAAAREQEQDKLGQQVNRKTNMSRFEAHMLQ
                                                                 SLKYDSRPGHIQTTKQISFQDQDSSSTQSTGQSYTEVASSGDDNPSRQISFSAKSGSE
ITQRKGFASNPKQGSMTGFPNIHFAPAQANFSFHYADPHYGGLLAATYLPQAPTCNPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="F3N23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .116944
                                                                                                                                                                                                                                                                                                                                                                                                                                   .8658,8746.
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join(16543...16961,17058...17907)

/gene="#73N23.5"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAKDPSWTGPGSRIIITTRDKGLLNSCGVNNIYEVKCLDDKDALQVFKKLAFGGRPPS
GGFEQLFIRASRLAHGLPSALYAFASHLSALYAIDEWEDELALLETPPQKNYQEILRA
SYDGLDQYDKTVFLHVAGFFRGRELKI IRAFKLKCDARIHLAKCLVNISIDGCISM
HILLVOTGREIVRQESDWRPSKQRELKYDFTEHHYVLOSNTHLGGNVSNLQLISDDVYL
SRNLKLLHWDAYFLTILPFIFRPHTIIELSLRYSKLNSLWDGTKLLPNLRILDVTGSR
NLRELPELSTAVNLEELILLESCTSLYQIPESINKLYLKKLNMYCDGLEGVILVNDLQ
EASLSRWGLKRIIILHFISGATLSSLTDLAIGKNIFKLSGTGDHLSFSSVQKTA
HOSVTHLLNGGFFGLKSLDIKRESYRLDPVNFSCLSFADFFCLTELKLILNIEDIPE
DICQLQLLETIDLGGNDFVYLPTSMGQLAMLKYLSLSNCRRLKALPQLSQVERLVLSG
CVKLGSLMGIIGAGRYNLLDFCVEKCKSLGSLMGILSVEKSAGRRNELLELSLENCKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"Similar to disease resistance proteins"
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NIKQLKEIVYLAHWFIPGSRVIFVTQDRNLLVESGVEHAYEQGLAYDEAALQLFSHSA
FDQQHPPTSFESLSLRAVHISGFLPLTLKILGSSLRGKDEERWEKELQQLEGDQEKAI
MEITSKRYTRAGKKEEDKEKITSFILLSDD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KYLPIFYGYKPSDYRYQEGSFATAFQSYDEADMIAEVYGGISSRLPRMKSTDLINLYG
MEAHMMKNTLLLNIGCEDEVHNIGIWGMGGIGKSTIAKCLYDRESRQFPAHCFLENVS
KGYDIKHLQKELLSHILYDEDVELWSNEAGSQEIKERLGHQKVEVVLDNYDKVEQLHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(12076. .12519,12613. .13851,13955. .14140, 14368. .15451,15672. .16057))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(12076. .16057)
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MIEEIYKD ISKKLLIMPOVDFSDIVGNNAHMENLSFLLSMDSINEVRHIGIWGKGGIG
KTTIAKCLFDDFSQGFBARCFLENVSKIYRKGGVSSLAEKFLSTTLGLSKKKMKGSGV
KLGPQEIKARFGCRKYFVYLDNYDDMAQMHAFAQESSNFGFGSRIIITTRDKGLLNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSSSSKFEVFLSFCSEDPSKTFVSVLDRWLEQKDITTNFKDDSF
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LAEPFQELGEGYPDDKIQEWRVSLTKLINIPALDSRYWSNEADMIELIANEILSISNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="Similar to part of downy mildew resistance protein RPP5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIQVPEPGDEIILCGVEHVGFVLK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WDCEGSRLYRINLKPNLYQSSEMMEDNNNRPYKWHHLVIVQIPTGIISAEIDEVQFES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYSISEELSHFTKLTYLDLSSLEFRRIPTSIRELSFMRTLYLNNCNKIFSLTDLPESL
KYLYAHGCESLEHVNFSSNHSFNHLDFSHCISLECISDLYRDFMNEEYSQEAPFRLVC
ITKYSIASTNNMRTSWREPMRIKLPKIKAAPKLVGFFVQIMVVCEKPFHLQFPAFSYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (gi|3860165),
(gi|3860163)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14368. .15451,1!
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FFRRWTSLKEWDDALCRFIEAPDESVMEILKISYDGLEETDKNVFLHVACLFNGEPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(19050. .23350)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(19050. .19667,19764. .21344,21686. .22799,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    resistance protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22887. .23350)
/gene="F3N23.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="F3N23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Similar
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                entire sequence of downy mildew
n RPP5 [Arabidopsis thaliana]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               downy mildew thaliana]
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Sd

gene

gene

Sgo

RATTLLDDGVLQGCLGLKILAEKSLIEITASGYIKMHNLVDQTARAIVNQESMQRRHG

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Matches 210;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84943 TTCA 84946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84523 CATCTGAAGCCACTCCATGTAACTGGTTTGGTATTATCTGTGATGATTCTAAGAAGGTTA 84582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  585 taca 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 caactettgttaateettgtaeettggteeetgtteaeetgttaaceaagaeaacegegtea 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCTTACTGGGGAATTGCCTAAATCCTTGTTTCGCATTCCGGTGTTGAATTATCTGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTCTCTCAACTTCACCGGTTCAGGTGTTTCAGGCCAATTGGGTCCTGAAATAGGGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctcgtgtggatttggggaaftcaaacctctctggacatcttgcgcctgagcttgggaagc 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGTCCCCGATACTCTCGGTAGCTTGAAGAGCTTGGCCGATTTGTATCTTTACAGCAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tagitcccacticttigggaaaattgaagictciggictititacggcitaatgacaacc 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTTAGGGAACTGTAGCTCACTTGTGTACATTGATTTGTCTGAAAATAGTTTCTCTGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aacttggaaatctgaagaatctcatcagcttggatctgtacaaccaatctttacaggga 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAAAAGCTTAGAGATATTGGATATGAGTTCTAACAATTTCTCTGGGATTATACCTTCCA 84702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ttgaacatttacagtatctagagctctacaaaaacaacatccaaggaactataccttccg 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGAGCATAACAACCTAACCGGGTTAATCCCTCAAAATGTTGGTGAAGCTAAGGAACTTC 84942
                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Convolvulaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ipomoea nil receptor-like protein kinase (inrpkl) gene, complete
                                                                                                                                                                             1 (bases 1 to 5033)
Bassett,C.L., Cohen,R.A., Nickerson,M.L. and Rajeevan,M.S.
Identification and Preliminary Characterization of an Unusual
Leucine-rich Repeat Receptor-like Protein Kinase from Morning
                          2 (bases 1 to 5033)
Bassett,C.L., Cohen,R.A., Nickerson,M.L. and Rajeevan,M.S
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ipomoea níl
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Japanese morning glory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INU77888
Submitted (12-NOV-1996) USDA, ARS, Appalachian Fruit Research
                                                                                                                                                                                                                                                                                                         [pomoea
                                                                                                                                                      Ipomoea nil)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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ILAIFLFFEYEYAQGMPNLRKLDLSDSRULEQLEDLSMAVNLEELITGGCKRLKKIPES
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NLQSLLELSIAEQDCGRFQWLELWYDGCKSIRSILDQLRHFIKLSYLDLSSHEFEKLP
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HCFGLKRDEHLIAQFLNEGENEEESLGFAFFPGTEVPSYFDHIDKGKSLTIDLPQIWP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ccagagctgggatccaactcttgttaatccttgttacctggttccatgtcacctgtaacca
AGAAACTGTTTATTTCACTGGCAATGGTCTTAATGGTTCAATCCCTTCAAA 1691
                                                                                                                          CTCAATTCCTTCCCAGCTAGGCAATTGCAGTCTTCTTGAACACATAGATCTGTCCTCCAA
                                                                                                                                                                                                                                                                                                                                   aactataccttccgaacttggaaatctgaagaatctcatcagcttggatctgtacaacaa
                                                                                                                                                                                                                                                                                                                                                                                         CGAAATCTCGCATTTGAAGCATTTGAAGAAGGTTGTTCTCAGTGGCAATGGTTTCTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGACAATTIGTTGATACTCTGAACCTCTCCTCTATGGAATCTCAGGCGAATTCGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agacaaccgcgtcactcgtggatttggggaattcaaacctctctggacatcttgcgcc
                                                                                                                                                                                           CAGCTTTACTGGTAATATCCCTGACACCCTTGGAGCTTTGCAGAATTTAAGGAACTTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                   tgagcttgggaagcttgaacatttacagtatctagagctctacaaaaacaacatccaagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205;
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PPGIGNCTSLREEGAFSCALGGPIPSCFGQLTKLDTLYLAGMIPSGRIPPELGKCKSM
IDLQIQQNOLEGSIPGELGMLSQIQVLHLYTTNNLSGBPPLSIMKIQSLQSLQLYQNNL
SGELPVDMTELKQLVSLALVENHETGVIPQDLGANSSLEVLDJTRNMFTGHIPDLCS
QKKLKRLLLGYNYLEGSVPSDLGGCSTLERLILEENNLRGGLPDFVBKQNLLFFDLSG
NNFTGPIPPSLGNLKNVTAITYLSSOCSTLERLILEENNLRGGLPTSKAULKNILKGILPSE
LSNCHKLSEIDASHNLLMGSIPSTLGSSLTELTKLSLGENSFSGGIPTSLFQSNKLLML
QLGGNLLAGDIPPVGALQALRSLNLSSNKLNGQLPIDLGKLKMLEELDVSHNNLSGTL
RVLSTIQSLTFINLSHCSLAMIVLGALAFITLFSLRFLFLKKKLVETGIKNGSP
STLRPCNNGSNTGAGGLSTLGTAMIVLGALAFITLFSLRFLFSAFLFLHCKKSVQEBAIGA
QEGDGSLLNKVLEATENLNDKYVLGKGAHGTIYKATLSPDKVYAVKKLVFTGIKNGSV
SMNREIETIGKVEHRNLLKLEEFWLREKGYGLLLYTTYMENGSLDHIGLGETATIOSG S
SMNREIETIGKVEHRNLLKLEEFWLREKGYGLLLYTTYMENGSLDHIGHTSNFLDWS
SMNREIETIGKVEHRNLLKLEEFWLREKGYGLLLYTTYMENGSLDHIGHTSNFLDWS
SMNREIETIGKVEHRNLLKLEEFWLREKGYGLLTYTTYMENGSLDHIGHTSNFLDWS
SMNREIETIGKVEHRNLLKLEEFWLREKGYGLLTYTTYMENGSLDHIGHTSNFLDWS
SMNREIETIGKVEHRNLLKGLEFWLREKGYGLLTYTTYMENGSLDHIGHTSNFLDWS
SMNREIETIGKVEHRNLLKGLEFWLREKGYGLLTYTTYMENGSLDHIGHTSNFLDWS
SMNREIETIGKVEHRNLLKGLEFWLREKGYGLLTYTYMENGSLDHIGHTSNFLDWS
SMNREIETIGKVEHRNLLKGLEFWLREKGYGLLTYTYMENGSLDHIGHTSNFLTWENGSLDHIGHTSNFLTURGSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRHNIAVGTAHGLAYLHFDCDPAIVHRDIKPMNILLDSDLEPHISDFGIAKLLDQSAT
SIPSNTVQGTIGYMAPENAFTTVKSRESDVYSYGVVLLELITRKKALDPSFNGETDIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mkyavntfllslcstssiyaafalnsdgaallsltrhwtpipsd
translation="mkyavntfllslcstssiyaafalnslgaetegelslkhlkkyvlsgn
gffgsipsqlghcsllselslssnstflnlslsstgtgetegelslkhlkkyvlsgn
lsiphletvfftgnglngsipsnignkelthukldngesgpvpsstgnittlgely
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/gene="inrpk1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="receptor-like protein kinase"
/protein_id="AAB36558.1"
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/cultivar="Violet"
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49.9%;
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1.1e-12;
hes 206;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                    249 acctetetggaeatettgegeetgagettgggaagettgaacatttacagtatetagage 308
CTATTCTTTATCTTTACGAGAACTATTTAACTGGTGTCATTCCCCCGGAACTAGGCAACA 2645
                                                                                                           totacaaaaacaacatocaaggaactataccttccgaacttggaaatctgaagaatctca 368
                                                                                                                                                                         ATCTAACTGGTGGCATTCCCCCGAAACTAGGCAACATAGAATCCATGATCGATTTAGAGT
                                      tcagcttggatctgtacaacaacaatcttacagggatagttcccacttctttgggaaaat 428
                                                                                    TGAGTAACAAACTTACCGGTTCAATTCCTTCTTCCTTAGGAAATCTCAAGAATTTGA
                                                                                                                                                                                                                                                               165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Street, Albany, CA 94710, USA
On Feb 11, 2000 this sequence version replaced g1:6693723.
The sequence is of BAC F14D7 from Arabidopsis thaliana chromosome
1. The sequence does not represent the sequence of the entire
insert of this clone. It is shorter by 6954 bp because we submit
only the unique sequence of the clone. However, in order to
facilitate the joining of overlapping clones in the future for
creation of larger contigs, we provide small overlaps (200 bp)
between overlapping sumbitted clones. The 5' end of this sequence
overlaps by 200 bp to the 3' end of the sequence of the clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 81513)
Liu,S.X., Sakano,H., Yu,G., Lee,J.M., Lenz,C., Pham,P., Torium,Chin,C., Chiou,J., Choi,E., Chung,M., Gonzalez,A., Howng,B., Liu,A., Vaysberg,M., Altafi,H., Brooks,S., Buehler,E., Chao,Q., Conn,L., Conway,A.B., Hansen,N.F., Johnson-Hopson,C., Khan,S., Kim,C., Lam,B., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R., Federspiel,N.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Street, Albany, CA 94710, USA 3 (bases 1 to 81513)
Theologie *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 overlaps by 200 bp to the 3' F1504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission Submitted (09-FEB-2000) Plant Gene Expression Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission Submitted (15-JAN-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana chromosome 1 BAC F14D7 sequence unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                        /clone="F14D7"
13814 c 13868 g 26052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .81513
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                                                                                                                                                                                                                                                             Score 79.8; DB 50;
Pred. No. 4.1e-12;
0; Mismatches 142;
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                                                                                                                                                                                                                                                                                                    Length 81513;
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                 Genes were identified by a combination of three methods: Gene prediction programs including GRAII (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/~chris/GENSCANW.html), and NetPlantGene (http://gnomic.stanford.edu/~chris/GENSCANW.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tigr.org/tdb/at/at.html). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       caatccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tgaagtototggtottttttacggottaatgacaacogattgacggggoccaatcocotagag 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lin,X. and Kaul,S.
Direct Submission
Submitted (14-OCT-1999) The Institute for Medical Center Dr. Rockville, MD 20850,
3 (bases 1 to 134402)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lin, X., Kaul, S., Town, C.D., Benito, M., Creasy, T.H., Ronning, C.M., Koo, H., Fujil, C.Y., Utterback, T.R., B. Bowman, C.L., White, O., Nierman, W.C. and Fraser, C.M. Arabidopsis thaliana chromosome I BAC FIM20 genomic Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete sequence. AC011765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr.
Rockville, MD 20850, USA
e-mail: xlin@ttgr.org
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Submitted (08-DEC-1999) The Institute for Genomic Research,
Submitted (08-DEC-1999) The Institute for Genomic Research,
Medical Center Dr., Rockville, MD 20850, USA
On Dec 8, 1999 this sequence version replaced g1:5102640.
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAC clone F1M20 is from Arabidopsis chromosome I and is near the molecular marker m1425.
The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lin, X
ittp://ftp.genome.washington.edu/RM/RepeatMasker.html). Regions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 134402)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for Genomic Research,
), USA, xlin@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic sequence,
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exons by
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1378. 1581

/note="exon predicted by xgrail, quality good_shadowexon" (complement(1509. 1530)

/note="exon predicted by xgrail, quality marginal" (complement(join(<1655. 1777,1908. 2135,2258. 2581, 2679. 2963,3052. .>3429))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mgcvsskqtvsvtpaidhsgvfkdnenecsgsgrivvedpprpt
LKKLVSWRSRSGKRRSQKSGSELGSESGRASDSLSFRLGNVSRYLEAEQVAAGWPAWL
SNVAGEAIHGWVPLRSDAFEKLEKIGQGTYSNVFRAVETETGRIVALKKVRFDNFEPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to p58 protein kinase GB:AAB59449 [Homo saplens]; contains Pfam profile: PF00069 Eukaryotic protein kinase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(<1655. .>3429)
/gene="F1M20.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1271. .1354
/note="exon predicted by xgrail,
complement(1356. .1475)
/note="exon predicted by xgrail,
                              /translation="MELADRAVGLLLSSISLSIFTYYTFWVIILPFVDSDHFIHKYFL PQDYALLVPVPAGIALLSLISVFIGMYMLKSKKKKA" complement(5111..5190) /note="exon predicted by xgrail, quality excellent" complement(<5342...>7603)
                                                                                                                                                                                                                                                                                                                                                                               /note-"similar to dolichyl-phosphate mannosyltransferase polypeptide 2 GB:4503365 [Homo sapiens] (regulator of dolichol phosphate-mannose synthesis: EMBO J 1998 Sep 1;17(17):4920-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HKRGTASSALVSQYFTTKPFACDPSSLPIYPPSKEIDTKHRDEAARSVISFIT" complement(4069. .4131)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVKEMAREILILARLNHPNIIKLEGLITSKLSCNIQLVFEYMEHDLTGLLSSPDIKFT
TPQIKCYMKQLLSGLDHCHSROYMHRDIKGSNLLLSNEGILKVADEGLANESNSSGHK
KKPLTSRVYTLMYRPPELLLGATOXHADIKSVGCVFAELLLGKPILKGRTISVEQLH
KIFKLCGSPPEDYWKKSKLPHAMLFKPQQTYDSCLRETLKDLSETEINLIETLLSIDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative protein kinase"
/protein_id="AAF15905.1"
/db_xref="GI:6539235"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(1655. .17
2679. .2963,3052. .3429))
/qene="F1M20.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="exon predicted by xgrail, 1271. .1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(744.
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complement(229. .281
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138. .269
                                                                                                                                                                                                                                          /product="putative dolichyl-phosphate mannosyltransferase
polypeptide 2"
                                                                                                                                                                                                                                                                                                                                 complement(join(4608. .4760,4885. .4974))
/qene="F1M20.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(<4608. .>4974)
/gene="F1M20.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="exon predicted by xgrail, quality excellent" complement(join(<4608. .4760,4885. .>4974))
/gene="FiR20.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="F1M20.
/codon_start=
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/chromosome="I"
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/db_xref-"GI:6539236"
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DVVCQWPGIICTPQRSKYTGINIJDSTISGPLFKNFSALTELIYLDLSRNTTEGEIPD
DLSRCHNLKKHLNLSHNILEGELSLPGLSNLEVLDLSLNRITGDIQSSFPLFCNSLVVA
NLSTNDFTGRIDD IFNGCRNLKYVDFSSNRFSGEVWTGGRILYEFSVADNHLSGNISA
SKFRCNCTLQMLDLSGNAFGGEFPGQVSNCQNLNVLNLWGRETGNIFSSLKSLKSKINGSALTELITALNITSRNID IFFILLNITNLYFIDLSRNKFGGDIQSLKFLILAYNNFSGDIPQEYCN
GGINSSNILKLPNLSGNLFSGNAFGGEFPGQVSNCQNLNVLNLWGRETGNIFSGDIPQEYCN
GGINSSNILKLPNLSGNLDFGYNNFSGDLFFEISQIQSLKFLILAYNNFSGDIPQEYCN
MPGLQALDLSFNKLTGSIPASFGKLTSLLWLMLANNSLSGEIFAREIGNCTSLLWFNVA
NNQLSGRFHPELTRWGSNFSFTFVNRQKDKIIASGSGLLAKKFWIIAFSGEIFASISGN
MPGLQALDLSFNKLTGSIPASFGKLTSLLWLMLANNSLSGEIFAREIGNCTSLLWFNVA
NNQLSGRFHPELTRWGSNFSFTFVNRQKDKIIASGSGELAKKFWIIAFSGEIFASISGN
DRLSTLHLGFNEFEGKLPFEIGQLPLAFLNLTRNNFSGEIFOZGLKCLQNLDLSFN
NNGLSGRFHPELTRWGSTFSTVRTLKASALQLJSGNKFSGEIFASISGN
DRLSTLHLGFNEFEGKLPFEIGQLPLAFLNLTRNNFSGEIFOZGLKCLQNLDLSFN
NGSGNFFTSLNDLNELSKFNISYNFFISALAFTGQVAFFDKDSFLGNFLARFSFFFN
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QSGNNTRKLSNQVLGNRFFTLLIWISLALAFTGQVAFFDKDSFLGNFLARFYVGRGGY
GTVYRGVLFDGREVAVKKLQREGTEREKTRADMEVLSANAFGDWAHIPNLYNLSGRGGY
GTVYRGVLFDGREVAVKKLQREGTEREKTRADMEVLSANAFGDWAHIPNLYNLSGULFGUFF
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RLKKRVKEDCINGKFSDLLKKVIARPETLEDAYDCIKLNSKYNSITERNGSVAPDSIAE
ELSGYFDVASNTES IVARDKTKEVLVLPSVALKVYQEAIRIVLSVVESPHESKISHS
ELSGYFDVASNTES IVARDKTKEVLVLPSVALKVYQEAIRIVLSVMEEKVEDSSLSILL
RSMFEARVLNLERGGFPKGHGLPQEGVLSRVLMNIYLDRFDHEFYRISMRHBALGLDS
KTDEDSPGSKLRSWFRQAGEQGLKSTTEDQLVAKKYVRESPYRAYMKLKEK
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KTDEDSPGSKLRSWFRQAGEQGLKSTTEDGLYVAKYVRESPYKAYMKLKEK
VRLFALQKEEAWTLGTVRIGKKWLGHGLKKVKESEIKGLADSNSTLSQISCHRKAGME
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SETJANLEALLPCYGGHDREVFFGDVVAFTHAIGRKLKFKYGLITAAKKRIHEMEIEKR
TOAQIIDWYSGLVRRWVIWYEGCSNFDEIKALINQIRNSCIRTLAAKKRIHEMEIEKR
LDLELSTIPSAEDIEQEIQHEKLDSPAEDRDEHTYGLSNGSICLLSLARTVSESRPC
LDLELSTIPSAEDIEQETQHEKLDSPAEDRDEHTYGLSNGSICLLSLARTVSESRPC
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9421. 9528
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/gene="F1M20.3"
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/note="exon predicted
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/protein_id="AAF15908.1"
/db_xref="GI:6539238"
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/note="exon predicted by xgrail,
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/protein_id="AAF15907.1"
/db_xref="GI:6539237"
                                                                                                                  VKASNVLLDKHGNARVTDFGLARLLNVGDSHVSTVIAGTIGYVAPEYGQTWQATTRGD
                                                                                                                                           DGSEKILVHEYMGGGSLEELITDKTKLQWKKRIDIATDVARGLVFLHHECYPSIVHRD
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                              Score 79.2;
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                              6.4e-12;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

June 23, 2000, 22:53:01 ; Search time 446.21 Seconds
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Post-processing: Minimum Match Listing first

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chosen parameters:

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N W09743427-A1.

P 13-MAY-1997; E02443.

F 13-MAY-1996; GB-010044.

R 14-MAY-1996; GB-010044.

A (NOVS) NOVARTIS AG.

De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;

R WPI: 98-086559/08.

R P-PSDB; W47020.

P Production of apomictic seeds - useful in plant breeding

C Claim 28; Pages 79-80; 123pp; English.

C The sequence is that of an EST clone showing high homology to

C SERK LRR (leucine-rich repeat) sequences.

C Sequence 788 BP; 234 A; 191 C; 156 G; 207 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V06588 standard; cDNA to mrNA; 788 BP.
V06588;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST clone.
receptor kinase; apomixis; apomictic; seeds; production; plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
Location/Qualifiers
CDS
CDS
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gaatctcatcagcttggatctgtacaacaacaatcttacagggatagttcccacttcttt
                                                              GAATTCAAACCTCTCTGGACATCTTGCGCCTGAGCTTGGGAAGCTTGAACATTTACAGTA
                                                                        gaattcaaacctctctggacatcttgcgcctgagcttgggaagcttgaacatttacagta
                               totagagototacaaaaaacaacatocaaggaactatacottocgaacttggaaatotgaa
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                    tctagagct()tacaaaaacaaccatccaaggaactataccttccgaacttggaaatctgaa
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20-NOV-1997.
13-MAY-1996; GB-010044.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, S
WPI; 98-08559/08.
P-PSDB; W47022.
                                                                                                                                                                                                                                                       plant breed1
Arabidopsis
Key
CDS
                                                                                                                       Production of apomictic seeds - useful in plant br Claim 28; Pages 86-88; 123pp; English.
The sequence is that of an EST clone showing high SERK LRR (leucine-rich repeat) sequences.
Sequence 1063 BP; 313 A; 242 C; 206 G;
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                                               CACATGGCGTCTCGAAACTATCGGTGGGAGCTCTTCGCAGCTTCGTTAATCCTAACCTTA
                                                         cccacgcgtccgcgaaactatcggtgggagctcttcgcagcttcgttaatcctaacctta
agtttaacagatccggaccatgttctccagagctgggatccaactcttgttaatccttgt
                        gctttgattcacctggtcgaagcaaactccgaaggagatgctctttacgctctttcgccgg
                 GCTTTGATTCACCTGGTCGAAGCAAACTCCGAAGGAGATGCTCTTTACGCTCTTCGCCGG
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(NOVS ) NOVARTIS AG.

De Vries SC, Hecht VFG, Schmidt EDL, Van Wpr; 98-086529/08.

P-PSDB; W47/019.

Production of apomictic seeds - useful in Claim 28; Pages 75-77; 123pp; English.

The sequence is that of an EST clone show SERK LRR (leucine-rich repeat) sequences
                                                            WO9743427-A1.
20-NOV-1997.
13-MAY-1997; E
14-MAY-1996; C
                                                                                                                       03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST receptor kinase; apomixis; apomictic; seeds; plant breeding; leucine-rich repeat; ss. Arabidopsis thaliana.
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GB-010044.
                                                                                          Location/Qualifiers
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Pred. No. 2e-2:
0; Mismatches
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                                                        production;
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20-WOV-1997.

20-WOV-1997.

R 14-MAY-1996; GB-010044.

R (NOVS) NOVARTIS AG.

I De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;

R WPI; 98-086529/08.

R P-PSDB; W47018.

T Production of apomictic seeds - useful in plant breed Claim 28; Pages 71-73; 123pp; English.

C SERK LERK (leucine-rich repeat) sequences.

Sequence 1106 BP; 331 A; 258 C; 206 G;
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Best I
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Local Similarity 96.2
hes 753; Conservative
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/note= "shows high ho
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1. No. 5.2e-206;
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Best Local S
Matches 538
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20-NOV-1997, E02443,
13-MAY-1996; GB-010044.
[NOVS] NOVARTIS AG.
De Vries SC, Hecht VFG, S
WPI; 98-08539/08.
P-PSDB; W47021.
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Arabidopsis thaliana SERK LRR homology
receptor kinase; apomixis; apomictic;
plant breeding; leucine-rich repeat;
Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Production of apomictic seeds - useful in plant br Claim 28; Pages 83-84; 123pp; English.
The sequence is that of an EST college high SERK LRR (leucine-rich repeat) sequences.
Sequence 894 BP; 270 A; 163 C; 176 G;
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les 538; Conserv
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ccctagagcactcactgcaatccccaagccttaaagttgttgatgtctcaagcaatgattt
                                                                                                 gggaaaattgaagtctctggtctttttacggcttaatgacaaccgattgacggggccaat
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thaliana SERK LRR homologous EST
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/note= "shows high homology to
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Pred. No. 1.8e-99;
D; Mismatches 110
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The sequence is that encoding SERK, a putative receptor kinase. The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity plant parts; and (c) expressing the sequence in the vicinity plant proyeny. This is useful in plant can be developed into plant proyeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides the case that sexual plants are available as crosses with the case that sexual plants are available as crosses with the propagated hybrids and could shorten and simplify the breeding programs of propagated hybrids and could shorten and simplify the breeding programs allows plant breeders to develop cultivars with Apomixis allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.

Sequence 2089 BP; 568 A; 419 C; 503 G; 599 T;
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(NOVS ) NOVARTIS AG.
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Production of apomictic seeds - useful in plant breeding production of apomictic seeds - useful in plant breeding production 21; Pages 47-51; 123pp; English.

Comprising: Is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nuclectide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced containing programs. Controllable and reproducible apomixis provides the case that sexual plant pargument and cultivar development in the case that sexual plants are available as crosses with the apomixic plant. Apomixis provides for true-breeding, seed propagated hybrids and could shorten and simplify the breeding containing and program testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with containing the plant traits for such characteristics as height,
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Sequence
DNA encoding plant morphogenesis regulatory protein - useful to yield plants with short stems or altered inflorescence Claim 1; Pages 6-10; 17pp; Japanese.

The present sequence encodes an Arabidopsis thaliana plant morphogenesis regulatory protein (MRP), which can be used to yield a plant with, e.g. short stems or altered inflorescence. The MRP acts on a plant at a specific site for a specific period, and can therefore be used to regulate extraneous gene expression in a plant. The MRP's CDNA or genomic DNA can be used to transform a plant to increase its MRP expression, and therefore control the form (particularly stem length) of the plant.

Sequence 3176 BP; 927 A; 654 C; 659 G; 936 T;
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Arabidopsis thaliana plant morphogenesis regulatory protein (
Plant; morphogenesis; regulation; short; stem; alteration;
Plant; morphogenesis; regulation; expression; transformation;
                                                                                                                                                                                                                                                                                                                                        24-AUG-1995; 216187.
24-AUG-1995; JF-216187.
(MITS-) MITSUI GYOSAI SHOKUBUTSU (CHIK-) ZH CHIKYU KANKYO SANGYO G WPI; 97-206629/19.
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10-JUN-1997
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increase; control; form; l
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Similarity

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Best Local Sin
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Matches 165; Conserv
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17-JUL-1998; U14841.
13-AUG-1997; US-910386.
(REGC) UNIV CALIFORNIA.
Hulbert SH, Richter T, Ro
                                                                                                                                                                                                                         New RRK polynuclectides and nucleic acid constructs - used for generating transgenic plants resistant to Xanthomonas Claim 1; Page 52-53; 67pp; English.
This invention describes a method for conferring disease resistance in plants. The invention describes the use of novel genes and proteins belonging to the Oryza longistaminata and Oryza sativa receptor kinase-like protein (RRK) Xa21 multigene family. Such genes from cassava, maize and tomato are also described. The genes and proteins ca be used for enhancing resistance to Xanthomonas in a plant, preferably rice or tomato.

Sequence 5940 Bp; 1570 A; 1200 C; 1188 G; 1982 T;
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Oryza
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WO9909151-A2.
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                                           GACCTCAGCGACAACCACCTGTCCGGCAAGATACCCTAGGAACTCAGCAGTCTCAGCAGG
                                                                    gagctctacaaaaacaacatccaaggaactataccttccgaacttggaaatctgaagaat
                                                                                                  ngistaminta Xa21 gene family member A2 DNA.
receptor kinase-like protein; multigene family; RRK; rice
disease resistance; cassava; maize; tomato; Xanthomonas;
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8.8e-13;
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11-MAY-1994; GB-009394.

23-DEC-1994; WO-G02812.

31-MAR-1995; GB-006658.

07-APR-1995; GB-007232.
                                                                                                                                                                                                                                                                                                                                                                                                Increasing plant pathogen resistance by induction of varisgation—may lead to acquired resistance to a broad range of pathogens.

Claim 9; Page 85-87; 131p; Engilsh.

T06307 is a tomato pathogen resistance gene Cf-2.2 partial cDNA clone. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagules of plants) containing such constructs. Cf-2.2 imparts resistance to the disease caused by the leaf mould fungal pathogen Cladosportum fulvum.

C.fulvum contains avirulence (Avr) genes that confer recognition by plants containing Cf-genes, leading to the activation of host defence mechanisms to attack the disease.

Sequence 3573 BP; 1032 A; 654 C; 664 G; 1223 T;
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CCGAGAAACAATTTGAAGGGAAAAGTTCCGCAATGTTTGGGTAATATCAGTAACCTTCAG
                         cttacagggatagttcccacttctttgggaaaattgaagtctctggtctttttacggctt 454
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Pred. No. 8.5e-12;
0; Mismatches 171;
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Matches 174
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11-MAY-1994; GB-009394.

23-DEC-1994; WG-GO2812.

31-MAR-1995; GB-00658.

07-APR-1995; GB-007232.

(GATS-) GATSBY CHARITABLE F

Hammond-Kosack KE, Jones D

WPI; 96-010949/01.

P-PSDB; R85298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Increasing plant pathogen resistance by induction of variegation - may lead to acquired resistance to a broad range of pathogens. Claim 9; Page 80-83; 131pp; English.

706306 is the tomato pathogen resistance gene Cf-2.1. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagules of plants) containing such constructs. Cf-2.1 imparts resistance to the disease caused by the leaf mould fungal pathogen Cladosporium fulvum. C.fulvum contains avirulence (Avr.) genes that confer recognition by plants containing Cf-genes, leading to the activation of host defence mechanisms to attack the disease.

Sequence 6471 BP; 2073 A; 1106 C; 1122 G; 2170 T;
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Pathogen resistant; Cf-2.1;
leaf mould; variegation; ds.
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wes 174; Conserv
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CTCATTGGGGAAATTCCTTCATCTGTGCAATTTGACATCACTGGAAGTGTTGTATATG 3710
                                   ataccttccgaacttggaaatctgaagaatctcatcagcttggatctgtacaacaacaat
                                                                                                                                                                                                         ATAGGTTACTTGAGTTCTCTTACTTATCTATCTTTGGGTAATAACTCTCTTAATGGACTT
                                                                                                                                                                                                                                                     cttgggaagcttgaacatttacagtatctagagctctacaaaaacaacatccaaggaact
                                                                                                                                                                                                                                                                                                         AACAACTTGTCTATGTTGTATCTTTACAATAATCAGCTTTCTGGCTCTATTCCTGAAGAA
                                                                                                                                                                                                                                                                                                                                                           aaccgcgtcactcgtgtggatttggggaattcaaacctctctggacatcttgcgcctgag
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5015. .647
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1677. .1745
/*tag=__c
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1677. .
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1. .1676
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l; tomato; C.fulvum; Avr 4;
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Pred. No. 1.1e-11;
0; Mismatches 171;
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production of apomictic seeds - useful in plant breeding claim 26; Pages 64-67; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant material and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant, Apomixis provides for true-breeding, seed propagated hybrids and could shorten and simplify the breeding
                                                                                                                                                                                                    20-NOV-1997.
13-MAY-1997; E02443.
13-MAY-1996; GB-010044.
(14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, S
WPI; 98-086529/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor kinase; apor
plant breeding; ds.
Arabidopsis thaliana
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Arabidopsis
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5295. .5803
/*tag= i
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/number= 6
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3851. .39
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apomixis; apomictic;
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Best I
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W09743427-A1.
20-N0V-1997, E02443,
13-MAY-1996; GB-010044.
(NOVS ) NOVARTIS AG.
De Vries SC, Hecht VFG, $
WPI; 98-086539/08.
P-PSDB; W47013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.

Sequence 4081 Bp; 1120 A; 770 C; 785 G; 1406 T;
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5295. .5803
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3851. .3979
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Pred. No. 1
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                                           Van Holst
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.4e-11;
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The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide comprising: (a) transforming plant material with a nucleotide cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant to breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with seed in the could stable traits for such characteristics as height, seed and forage quality and maturity.

Sequence 6695 BP; 1844 A; 1182 C; 1243 G; 2422 T;
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Best Local :
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Key
CDS
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20-MAY-1998
CF-5 pathoge
Claim 3; Fig la; 75pp; English the polynucleotide of the inventic This sequence is an example of the polynucleotide of the inventic is able to confer pathogen resistance on a plant. It is one of two cressives of the pathogen consistence against the pathogen cladosporium fuluum-5. Transgenic plants can be produced by incort the gene into plant cells and regenerating plants from the cells; as executably or sexually produced offspring can also be subsequently
                                                                                                  Tomato gene Cf-5, confers resistance to Cladosporium fulvum - useful for production of transgenic plants resistant to pathogens e.g. tomato leaf mould C. fulvum in tomatoes Claim 3; Fig la; 75pp; English.
                                                                                                                                                                          P-PSDB; W41309
                                                                                                                                                                                       09-MAY-1996; GB-009681.
(INNE-) INNES CENT INNOVATIONS LTD JOHN.
Dixon MS, Hatzixanthis K, Jones DA, Jone
WEI; 98-008895/01.
                                                                                                                                                                                                                                               24-SEP-1996;
09-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                    CF-5 pathogen resistance gene variant #1.
Tomato; CF-5 pathogen resistance gene; Clade tomato leaf mould; Phytophthora resistance;
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08-MAY-1997;
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Pred.
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No. 1
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.7e-11;
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Best Local S
Matches 172
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20-ROV-1997; G01249.
08-MAY-1997; G01249.
24-SEP-1996; GB-019924.
09-MAY-1996; GB-009681.
(INNE-) INNES CENT INNOVATIONS LTD JOI DIXON MS, HALZIXANTHIS K, JONES DA, JOHP J98-008895/01.
Tomato gene Cf.5, confers resistance to Cladosporium fulvum - useful for production of transgenic plants resistant to pathogens e.g. tomato leaf mould C. fulvum in tomatoes

Claim 6; Fig 1b; 75pp; English.

This sequence is an example of the polynucleotide of the invention, is able to confer pathogen resistance on a plant. It is one of two to CF-5 gene variants, which offer resistance against the pathogen Cladosporium fulvum-5. Transgenic plants can be produced by incorpor the gene into plant cells and regenerating plants from the cells; assexually or sexually produced offspring can also be subsequently produced. Expression of the gene in plant cells can confer pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                         CF-5 pathogen resistance gene variant #2.
Tomato, CF-5 pathogen resistance gene, Clad
tomato leaf mould, Phytophthora resistance,
Lycopersicon pimpinellifolium.
Lycopersicon pimpinellifolium.
Lycopersicon pimpinellifolium.
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V14519;
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pathogen resistance gene; Cladosporium
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Pred. No. 1.6e-11;
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Best Local
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GTGTTGTATATGTCGAGAAACAATTTGAAGGGAAAAGTTCC
                      gttgttgatgtctcaagcaatgatttgtgtgtggaacaatccc
                                                                          AGTGATAACGATCTCATTGGGGAAATTCCTTCATTTGTGTGCAATTTGACATCACTGGAA
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Pred. No. 1.6e
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Job time: 40593 se June 23, 2000,

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Title:
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Listing first 45 summaries
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Maximum DB seq length: 1000000
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
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Match
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-238-163-3
US-08-527-680A-1
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US-08-566-271-4
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Sequence I, Appli		Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	•	Sequence 16, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 22, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Patent No. 5340934

ALIGNMENTS

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Sequence 3, Application Patent No. 5952485
GENERAL INFORMATION:
APPLICANT: Ronald
                                                                                               REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0330
TELECOMMUNICATION: TOCKWATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NOWBER: US/08/567,375
FILING DATE: 04-DEC-1995
CLASSIFICATION DOTA:
APPLICATION NUMBER: US 60/004,645
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
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APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                   FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastien, Kevin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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CITY: San Francisco
                   LENGTH: 3921 base pairs TYPE: nucleic acid STRANDEDNESS: single
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    Application US/08567375
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; LOCATION: join(1..2676, 3520..3918)
; OTHER INFORMATION: /product- "Xa-21"
US-08-567-375-3
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US-08-587-680A-3
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             COMPTTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/587,680A
FILING DATE: 17-JAN-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08587680A Patent No. 5977434
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.1%;
Best Local Similarity 50.3%;
Matches 156; Conservative
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APPLICANT:
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APPLICANT:
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 27
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STATE: California
  APPLICATION NUMBER:
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Song, Wen-Yuang
Szabo, Veronique
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Pred. No. 7.1e-11;
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                                                                                                                                                                                                                                                                                                             RESULT 3
US-08-475-891A-3
                                                                                                                                                                                                                                                                      Sequence 3, Application US/08475891A Patent No. 5859339
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--- Tocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 0
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                      APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                      1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1279
COMPUTER READABLE FORM
                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308
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STRANDEDNESS:
TOPOLOGY: lin
                   COUNTRY:
ZIP: 941
                                                  STREET: Two Embarcac
CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                     CCAATACCCA 1468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atcagcttggatctgtacaacaacaatcttacagggatagttcccacttctttgggaaaa 427
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                   94111-3834
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                                    USA
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Pred. No. 7
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.1e-11;
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RESULT 4
US-08-238-163-3
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                                                                       Sequence 3, Application US/08238163
Patent No. 5569830
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
  APPLICANT:
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                                    APPLICANT:
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: si
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                                                                                                                                                                                                                                               acaatcccaa 557
                                                                                                                                                                                                                                                                                                                    gcactcactgcaatcccaagccttaaagttgttgatgtctcaagcaatgatttgtgtgga 547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCTGCAACAACTTTCAGAGGGTCTCTTCCATCATCGTTGGGCAGGCTTAAAAACTTA 1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 8.1%;
Similarity 50.3%;
56; Conservative
POWELL, Ann
STOTZ, Henrik
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RMATION: /product= "RRK-B"
RWATION: /note= "Ra21 Xanthomonas spp. disease
RWATION: resistance gene RRK-B from rice (Oryza
RWATION: sativa)"
                                  BENNETT, Alan
LABAVITCH, John M.
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Pred. No. 9.1e-11;
0; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5992;
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US-08-238-163-3
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin '
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Best Local Similarity 50.5%;
Matches 196; Conservative
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REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-9043
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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932 ATCGTAACANACTCACCGGAACAATACC
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STRANDEDNESS: SI
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
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                                                                                                                                                                                                                                                                                                                 atttacagtatctagagotctacaa---aaacaacatccaaggaactataccttccgaac 347
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                                                                                                                                                                                                                                       ttggaaatctgaagaatctcatcagcttggatctgtacaacaacaatcttacagggatag
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                              caagcaatgatttgtgtggaacaatccc
                                                                   TTACCGGAACAATCCCTTCTCTCTCTCAGCTTCCGAATTTGCTAGCGATGTACTTAG
                                                                                                    tgacggggccaatccctagagcactcactgcaatcccaagccttaaagttgttgatgtct
                                                                                                                                                                                                                TTGCGAAGCTCACAAATCTCAAAATGTTAAGGCTCAGCTTCACTAACCTTACAGGTCCGA 811
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Pred. No. 3.3e-09;
0; Mismatches 185; Indels
959
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US-08-587-680A-24

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                                                                                                                                                                                                                                                           Query Match 7.1%;
Best Local Similarity 49.5%;
Matches 144; Conservative
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APPLICANT: Wang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 576-03 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US
FILING DATE: 29-SEP-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATE: 07-JUN - FILING DATE: 07-JUN - PRIOR APPLICATION DATA: US 60/004,645
APPLICATION NUMBER: US 60/004,645
APPLICATION NUMBER: 29-SEP-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-058940US
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION NUMBER: US 08/373,375
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pair
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PITLE OF INVENTION: Proceduate TITLE OF INVENTION: Disease Resistance

TITLE OF SECULENCES: 27
                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLICANT:
                                                                                                                                                   310
                                                                                                                                                                                                               250 cctctctggacatcttgcgcctgagcttgggaagcttgaacatttacagtatctagagct 309
430 gaagtetetggtetttttaeggettaatgaeaacegattgaeggggeeaateeetagage 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 17-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/O
FILING DATE: 17-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                 cagcttggatctgtacaacaacatcttacagggatagttcccacttctttgggaaaatt 429
                                                                                                                                       ctacaaaaacaacatccaaggaactataccttccgaacttggaaatctgaagaatctcat 369
                                                                                                            AACTGGAAATGGTTTCTCAGGTGATATCCCTTCTGATATTGGCAGACTAAAGAGCATCTT 137
                                                                                                                                                                                    CTTGTCTGGTGCACTTCCTAGTGCTATTGGAAACTATTCAGGGCTGAAGAATCTTGTGTT 77
                                      AAAGCTGGACCTGAGTAGAAACAACTTCTCTGGCACAATCCCTCCTCAGATTGGTAACTG 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (415)
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                                                                                                                                                                                                                                                                                                                                                                        cDNA (partial)
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04-DEC-1995
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                                                                                                                                                                                                                                                                               Score 55.8; DB 4;
Pred. No. 1.5e-08;
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; NAME/KEY: misc_feature
; LOCATION: 1..1058
; OTHER INFORMATION: /standard_name= "Pear PGIP cDNA"
US-08-238-163-1
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US-08-238-163-1
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                                                                                                                                                                                     Query Match 7.0%;
Best Local Similarity 51.4%;
                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Rele-
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 03-MAY-199
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 543-504
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PLANT INHIBITORS OF TITLE OF INVENTION: POLYGALACTURONASES A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                    301
                                                                                                                                  241 gaattcaaacctctctggacatcttgcgcctgagcttgggaagcttgaacatttacagta 300
361 gaatctcatcagcttggatctgtacaacaaccatcttacagggatagttcccacttcttt 420
                                                                                                      342 GCAACCCAATCTCACTGGCCCAATCCAACCCGCCATTGCCAAGCTCAAAGGACTCAAGTC 401
                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1058 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                           totagagototacaaaaacaacatocaaggaactatacottocgaacttggaaatctgaa 360
                                                                                                                                                                          128;
                                     TCTCAGGCTCAGCTGGACCAACCTCTCAGGCTCTGTCCCTGACTTCCTCAGCCAACTCAA
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Steuart Street T
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STOTZ, Henrik
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                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34,774
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Tower, One Market Plaza
                                                                                                                                                                        0;
                                                                                                                                                                                       Score 55.4;
Pred. No. 1
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                                                                                                                                                                        Mismatches
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AND THEIR USE TO CONTROL FUNGAL DISEASE
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RESULT 7
US-08-475-891A-1
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REGISTRATION NUMBER: 34,774

REFERENCE/DOCKET NUMBER: 02370

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEPAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
TYPE: nucleic acid
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                                                                                 Matches 165;
                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/475.891;
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA: 800
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ronald, Pameta (APPLICANT: Wang, Guo-Liang APPLICANT: Song, Wen-Yuang
      2735
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                            NAME/KEY: CDS
LOCATION: join(1648..4383, 5178..5513)
COTHER INFORMATION: /product= "RRK-F"
OTHER INFORMATION: /note= "xa21 Xanthomonas spp. disease
OTHER INFORMATION: resistance gene RRK-F from rice (Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 ccctagage 489
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                      231 tggatttggggaattcaaacctctctggacatcttgcgcctgagcttgggaagcttgaac 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: Sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
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TGGACTTGGGAGAAAATAACCTGGGGGGGAGTTCTTCCTAATTCGTTTTCCAATCTTTCCA 2794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94111-3834
                                                                                                Similarity
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                                                                               Conservative
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                                                                                                7.0%;
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                                                                           Score 55.4; DB 3;
Pred. No. 4.5e-08;
0; Mismatches 161;
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                                                                                                                Length 6256;
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Patent No. 5952485
                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Ronald
                                                                                                                     TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pair
                                                                                                                                                            REGISTRATION NUMBER: 34,774
REFERENCE/COCKET NUMBER: 0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                               FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FITLE OF INVENTION: Procedures and Materia FITLE OF INVENTION: Disease Resistance in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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    MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08 FILING DATE: 04-DEC-1995
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                   STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                nucleic acid
DEDNESS: single
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                                                                                                                                                                                                                                           Bastian, Kevin L
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Song, Wen-Yuang
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                       linear
DNA (genomic)
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17-JAN-1995
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RESULT 9
US-08-587-680A-1
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Best Local Sim
Matches 165;
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                                                     SOFTWARE: PatentIn Release #1.0, Ver-
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,680A
FILING DATE: 17-JAN-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
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NAME/KEY:
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ronald, Pamela C.
APPLICANT: Rang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Disease Resistance in Plants
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             PRIOR APPLICATION NUMBER: US 08/475,891
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OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834
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RMATION: /product= "RRK-F"
RMATION: /note= "Xa21 Xanthomonas spp. d:
RMATION: resistance gene RRK-F from rice
RMATION: (Oryza sativa)"
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07-JUN-1995
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                                                                                                                                                                                                         Release #1.0, Version #1.30
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Pred. No. 4.5e-08;
0; Mismatches 161;
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NAME/KEY: CDS

LOCATION: Join(1648...4383, 5178...5513)

CHER INFORMATION: /product- "RRK-F"

OTHER INFORMATION: /note- "Xa21 Xanthomonas spp. disease

OTHER INFORMATION: resistance gene RRK-F from rice (Oryza

OTHER INFORMATION: sativa)"

US-08-587-680A-1
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US-08-473-553A-1
                                                                                                                                                                                         Sequence 1, Application Patent No. 5859338 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                              APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic
TITLE OF INVENTION: Transformed Plants, and
                                                                                                                                                                                                                                                                                                                                           3035
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APPLICATION NUMBER: US 6
FILING DATE: 29-SEP-1995
                    NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach,
                                                                                                                                                                                                                                                                                                                                                                                                                             2975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
  STREET:
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                                                                                                                                                                                                                                                                                                                                           GCACCAACAATTCAGTGGTTGGATACCA 3063
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  Four Embarcadero
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h, Test, Albritton & Herbert
Center, Suite 3400
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Pred. No. 4.5e-08;
0; Mismatches 161;
                                                                                     eic Acids,
and Proteins
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San Francisco

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US-08-473-553A-1
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                                                                                                                                                                            US-08-567-375-15
                                                                                                                                      sequence 15, Application US/08567375 Patent No. 5952485
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5733 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION UNMER: 38,304
REFERENCE/DOCKET NUMBER: A-60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                       GENERAL INFORMATION:
                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A
FILLING DATE: 06-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3120 CTACTACAACAGCTACACCGGTGGTGTTCCACGCGAGTTCGGTGGTTTAACAAAGCTTGA 3179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: FEATURE:
                                                                                                                                                                                                                                                                                                                        3240 GAAACATCTACATACTCTGTTTCTTCACATCAACAACTTAACCGGTCATATACCACCGGA 3299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3180 GATCCTCGACATGGCGAGCTGTACACTCACCGGAGAGATTCCGACGAGTTTAAGTAACCT 3239
           APPLICANT: Szabo, 1
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                APPLICANT:
                                                                                                                                                                                                                                                  3360 AATCCCTCAAAGC 3372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                          430 gaagtctctggtctttttacggcttaatgacaaccgattgacggggccaatccctagagc 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370 cagcttggatctgtacaacaacaatcttacagggatagttcccacttctttgggaaaatt 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 ctacaaaaacaaccatccaaggaactataccttccgaacttggaaatctgaagaatctcat 369
                                                                                                                                                                                                                                                                               550 aatcccaacaac 562
                                                                                                                                                                                                                                                                                                                                              490 actcactgcaatcccaagccttaaagttgttgatgtctcaagcaatgatttgtgtggaac 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States ZIP: 94111-4187
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Wang, Guo-Liang
Song, Wen-Yuang
Szabo, Veronique
WENTION: Procedures and Materials for Conferring
WENTION: Disease Resistance in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                   Ronald, Pamela C.
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5117..5467
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2434..5037
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Pred. No. 2.6e-07;
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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: I
US-08-567-375-15
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US-08-666-271-4
                     RESULT
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Best Local Sim
Matches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEPHAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/
FILING DATE: 07-JUN-1995
PRIOR APPLICATION UNMER: US 08/
PRILING DATE: 17-JAN-1995
FILING DATE: 17-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESSE: Townsend and Townsend and Crew LLP
ADDRESSEE: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACT
LENGTH: 831 k
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                                                                       273
                                                                                                      495
                                                                                                                                       213
                                                                                                                                                                       435
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                                                                                                                                                                                                                                           375
                                                                                                                                                                                                                                                                                            315 aaaacaacatccaaggaactataccttccgaacttggaaatctgaagaatctcatcagct 374
                                                                                                                                                                                                                                                                                                                                                                  255 ctggacatcttgcgcctgagcttgggaagctttgaacatttacagtatctagagctctaca 314
                                                                                                                                                                                                                                                                        93 GAAATGGTTTCTCAGGTGATATCCCTTCTGATATTGGCAGCTAAAGAGCATCTTAAAGC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                   TGGACTCGAGTAGAACTACTTCTCTGGCACAATCCCTCCTCAGATTGGTAACTGTCTTT 212
                                                                     CTCAAATTCACATCTTAAATTACATCAATATTTCCTGGAATCACTT
                                                                                                  ctgcaatcccaagccttaaagttgttgatgtctcaagcaatgattt 540
                                                                                                                                                                  ctctggtctttttacggcttaatgacaaccgattgacggggccaatccctagagcactca 494
                                                                                                                                                                                                                                      tggatctgtacaacaacaatcttacagggatagttcccacttctttgggaaaattgaagt 434
                                                                                                                                                                                                                                                                                                                                          CTGGTGCACTTCCTAGTGCTTTTGGAAACTATTCAGGGCTGAAGAATCTTGTGTTAACTG
                                                                                                                                     CCTTAACTTACTTGGATTTGAGCCAAAATCAACTTTCTGGTCCTATCCCAGTTCAAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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Pred. No. 4.4e-07;
0; Mismatches 147;
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                                                                                                                                                                                                                                                                                                                                                                                                               147;
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Sequence 4, Application US/08666271 Patent No. 5920000

GENERAL INFORMATION:

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNDER: PCT/GB94/02812
FILING DATE: 23-DEC-1994
PRIOR APPLICATION DATA:
                                                                          2253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: GB 9326428.1 FILING DATE: 24-DEC-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9409363.0 FILING DATE: 11-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                          2133 TGGACTTCGTACGTTGAACTTGTCTCACAATGTCTTGGAAGGTCATATACCGGCATCATT 2192
                                                                                                                                                                                                                                                                                                  2073 TATCAATCTCTCAAAGAACAGATTTGAAGGTCATATTCCAAGCATTATTGGAGATCTTGT 2132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 620-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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2313 TGTTGGATGCATCCCCAAAGGAAAACAATTTGAT 2346
                                                                                                                                                  2193 TCAAAATTTATCAGTACTCGAATCTTTGGATCTCCTAATAAAATCAGCGGAGAAAT 2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 11-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                        301 totagagototacaaaacaacatocaaggaactatacottocgaacttggaaatotgaa 360
                                  541 gtgtggaacaatcccaacaaacggaccttttgct 574
                                                                                                                                                                                    421 gggaaaattgaagtctctggtctttttacggcttaatgacaaccgattgacggggccaat 480
                                                                                                                                                                                                                                                            361 gaatctcatcagcttggatctgtacaacaacaatcttacagggatagttcccacttcttt 420
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                                                                          22201
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1100 NORTH GLEBE ROAD, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2880 base pairs
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HAMMOND-KOSACK, KIM E
THOMAS, COLWYN M
                                                                                                                                                                                                                                                                                                                                                                          6.1%;
llarity 48.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                              Score 48.4; DB 4; Pred. No. 5.5e-06;
                                                                                                                                                                                                                                                                                                                                                                            Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 2880;
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2913 TATCAATCTCTCAAAGAACAGATTTGAAGGTCATATTCCAAGCATTATTGGAGATCTTGT 2972

361 gaateteateagettggatetgtaeaaeaacaatettaeagggatagtteecaettettt 420

301 tctagagctctacaaaaacaacaacatccaaggaactataccttccgaacttggaaatctgaa 360

Gaps

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; NAME/KEY:
; LOCATION:
US-08-666-271-1
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                                                                                                                                                                                                                                                                                                    TELEFAX: 703-816-4100 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3905 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PILING DATE: 23-DEC-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326428.1

FILING DATE: 24-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9409363.0

FILING DATE: 11-MAY-1994

ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, R.T
Query Match 6.1%;
Best Local Similarity 48.5%;
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08666271 Patent No. 5920000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/UB/000,2,...
FILING DATE: 19-SEP-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PCT/GB94/02812
                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 62
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 703-816-4100
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HAMMOND-KOSACK, I
APPLICANT: THOMAS, COLWYN M
APPLICANT: JONES, DAVID A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UZIP: 22201
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                                                                                                                                                            LOCATION:
                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                              NAME/KEY:
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1100 NORTH GLEBE ROAD, 8TH FLOOR
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898..3489
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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898..966
                                                                                                                                                          mat_peptide
967..3486
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Score 48.4; DB 4;
Pred. No. 6.6e-06;
0; Mismatches 141;
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                                  Length 3905;
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US-08-244-646-14
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INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 1116 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 5744697
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: IT RM 91A 000915
FILING DATE: 06-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/IT/00158
FILING DATE: 04-DEC-1992
ATTOONNEY/AGENT INFORMATION:
NAME: SUllivan, Sally A.
REGISTRATION NUMBER: 32,064
REGISTRATION NUMBER: 32,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Releaction DATA:

APPLICATION NUMBER: US/C
FILING DATE: 06-JUN-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
                                                                                      MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleotide Sequences Coding An TITLE OF INVENTION: Endopolygalacturonase Inhibitor NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                      ORIGINAL SOURCE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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lambda PGIP-3.3
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Albersheim, Peter
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RESULT 15
US-08-592-936B-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 117; Conserv
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GENERAL INFORMATION:
                                                    TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 2917 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,936B
FILLING DATE: 29-DAN-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Evans, Susan T.
REGISTRATION NUMBER: 38,443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kellogg, Jill A.

APPLICANT: Bestwick, Richard K.

TITLE OF INVENTION: PLANT TISSUE / STAGE SPECIFIC PROMOTERS FOR TITLE OF INVENTION: REGULATED EXPRESSION OF TRANSGENES IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                   REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
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                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 350 Cambridge Avenue, Suite 250 CITY: Palo Alto
               TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTCTATATCACTCACACCAATGTCTCCGGCGCAATACCCGATTTCTTGTCACAGATCAA 461
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1027..1116
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Pred. No. 0.00062;
0; Mismatches 126;
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; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: ;
; INDIVIDUAL ISOLATE: ;
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Search completed: June 23, 2000, 22:45:40 Job time: 40286 sec
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                                                                                     1947 CCC 1949
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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611 361 670 418 418 992868 992868 FINITION	Qy 431 aagtetetggtetttttacggettaatgacaaccgattgacgggecaatccctagagca 490	Oy 251 ctctctggacatcttgcgcctgagcttggaaagcttgaaacatttacagtatctagagctc 310	Quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but acrial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using BASE COUNT 151 a 118 c 123 g 146 t 18 others ORIGIN Query Match Best Local Similarity 94.4%; pred. No. 1.1e-98; Matches 441; Conservative 0; Mismatches 20; Indels 6; Gaps 3;	Michigan State University, Plant Biology Bldg., E. MISU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing.Mi Tel: 517-353-0854 Fax: 517-353-0854 Fax: 517-353-9168 Email: 22313tcn@lbm.cl.msu.edu Seq primer: T7 dye primer: Location/Qualifiers 1. 556 /organism="Arabidopsis thaliana" /strain="var columbia" /strain="var columbia" /clone="1874577" /clone="1874577" /clone="1874577" /clone="1874577" /clone="1874577" /clone="1874577" /clone="1874577" /clone="1874577" /clone="1874577" /clone="1874577" /clone="1874577" /clone="1874577" /clone="1874577" /clone="1874577" /clone="1874577" /clone="1874577" /clone="1874577"	MEDLINE 95148729 COMMENT On Apr 14; 1993 this sequence version replaced gi:693023. Contact: Thomas Newman

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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On Dec 20, 1
Contact: Dav
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A1992868
A1992868.1 GI:5839773
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Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733
Fax: 314-427-3324
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/clone="101493826"
/clone=11b="A. thaliana, Ohio State clone set"
/note="CDNA, library was made from selected clones
Arabidopsis thaliana Ohio State clone set."
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Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, Retzel, E. and Somerville, C.
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The sequence entry for this EST has been reverse
is being submitted in the sense orientation.
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Tel: 517-353-0854
Fax: 517-353-9168
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/strain="var columbia"
/db_xref="taxon:3702"
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33803 Lambda-PRL2
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On May 5, 1995 this sequence version Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan State University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: 22313tcn@ibm.cl.msu.edu
The sequence entry for this EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 517-353-0854
Fax: 517-353-9168
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        Conservative
                                                                                                            /notes vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; /notes vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; /Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated eticlated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA. "

10 a 74 c 66 g 93 t 5 others
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Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
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Tel: 517-353-0854
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                /note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and
 siliques.
                                                                                                                                                         /organism="Arabidopsis
/strain="var columbia"
/db_xref="taxon:3702"
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The vector is
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 BRL's lambda Zip-Lox.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGGAGGGNCCGGANTTACTCGGTCTTGCAAGNTACGGCACTAACTGCANCTG
                                                                                       Lansing, Mi
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm
Seg primer: T7.
                                                                                                                                                            Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E. and Somerville,C.

Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones plant Physiol. 106, 1241-1255 (1994)

95148799

On May 18, 1995 this sequence version replaced gi:811121.

Contact: Thomas Newman
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E.

MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E.
                                                                                                                                                                                                                                                                                                                                                                                 Arabhidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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AA394359.1 GI:2047570
EST.
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25942 Lambda-PRL2
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1 (bases 1 to 534)
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                                                                                                        22313tcn@ibm.cl.msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inserts were directionally cloned with Sal-Not arms oligo dT primed cDNA. "
a 85 c 67 g 89 t 14 others
/organism="Arabidopsis
/strain="var columbia"
/db_xref="taxon:3702"
/clone="305G1T7"
                                                                            Location/Qualifiers
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94.1%;
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Arabidopsis thaliana
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Pred. No. 4.6e-80;
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                                             thaliana"
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305G1T7 3',
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REFERENCE
AUTHORS
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AW443205
LOCUS
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Best Local Sim
Matches 374;
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Lycopersicon.

1 (bases 1 to 608)

D'Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T.,
Liang,F., Hansen,T.S., Ronning,C.M., Craven,M.B., Bowme
Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,
Glovannoni,J.J. and Martin,G.B.
Generation of Essas from tomato callus (mixed elicitor)
                                                                                                                                           Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                             AW443205 608 bp mRNA
EST308135 tomato mixed elicitor, I
clone cLET43M10 5', mRNA sequence
AW443205
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                                                                                                                                                                                                                                     tomato
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/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA.

51 a 114 c 125 g 126 t 18 others
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Pred. No. 8.1e-80;
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                                                                      Bowman, C.L.,
                                                                                                                                                                                                                                                                                                                                   esculentum cDNA
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                                                                                          Holt, I.E.,
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Matches 401;
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                                                                                  GTAAAGGGGAATTCAGAAGGGGATGCTTTGTACGCCCTCCGCCGGAGCTTATCTGACCCG
                                                                                                                                                                           atcccaagccttaaagttgttgatgtctcaagcaatgatttgtgtggaacaatcccaaca 559
                                                                                                                                                                                                                                                                                                               ctgtacaacaactcttacagggatagttcccacttctttgggaaaattgaagtctctg 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                        catcttgcgcctgagcttgggaagcttgaacatttacagtatctagagctctacaaaaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acctgtaaccaagacaaccgcgtcactcgtgtggatttggggaattcaaacctctctgga
                                                                                                                                                                                                                                               CTGTACAACAACAATATTTCGGGGACAATTCCTACTTCACTTGGAAAACCTGAAAAACCTT
                                                                                                                                                                                                                                                                                                                                                                                              aacatccaaggaactataccttccgaacttggaaatctgaagaatctcatcagcttggat 379
                                                                                                                                                                                                                                                                                                                                                                                                                                    CATTTGGTACCTGAGCTCGGAAAGCTTGAACATCTACAGTATCTGGAGCTTTACAAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTTGCAACGGAGATAATCAAGTTACTCGTGTGGATCTTGGGAACTCAAAGTTATCTGGT
                                                                                                                                                                                                                             GTTTTCTTGCGTCTAAATGATAACAAGCTAACAGGACCAATCCCAAGAGAACTTACTAGC 488
                                                                                                                                                                                                                                                                                                                                                                  AATATTCACGGAACCATCCCTAAGGAGCTCGGTAACTTGAAGAGCCCTTATTAGTCTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Dec 20, 1995 this sequence version Contact: David Frisch Clemson University Genomics Institute Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 Jordan Hall,
 AW031110
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864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="4-6 week old plants"
/lab_host="XL1-Blue MRF',"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2
Xho1; cLET - Inoculated with a variety of disease respo elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenthion, EIX, okadaic acid, or systemin prior to tissue harvest. Eco site was destroyed during cloning."

a 126 c 134 g 183 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="cLET43M10"
/clone_lib="tomato mixed elicitor,
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cultivar="Rio Grande PtoR"
/db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Lycopersicon esculentum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1995 this sequence version replaced gi:1135853.
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Pred. No. 2.2e-77;
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                                                                                                                                                                                                                                         GTAAAGGGGAATTCAGAAGGGGATGCTTTGTACGCCCTCCGCCGGAGCTTATCTGACCCG 242
                                                                                                                                                                                                                                                                                                                                 gtcgaagcaaactccgaaggagatgctctttacgctcttcgccggagtttaacagatccg 139
 ctgtacaacaactcttacagggatagttcccacttctttgggaaaattgaagtctctg
                                                      aacatccaaggaactataccttccgaacttggaaatctgaagaatctcatcagcttggat
                                                                                                                        catcttgcgcctgagcttgggaagcttgaacatttacagtatctagagctctacaaaaac 319
                                                                                                                                                                                            acctgtaaccaagacaaccgcgtcactcgtgtggatttggggaattcaaaacctctctgga
                                                                                                        CATTTGGTACCTGAGCTCGGAAAGCTTGAACATCTACAGTATCTGGAGCTTTACAAAAAT
                                                                                                                                                                           ACTTGCAACGGAGATAATCAAGTTACTCGTGTGGGATCTTGGGAACTCAAAGTTATCTGGT
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AW031110.1
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cLEC13C21
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Alcala,J., Vrabalov,J., White,R., Matern,A.L., Vision,T.,
Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L.,
Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 Jordan Hall, (Tel: 864 656 4366 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
On Dec 20, 1995 this sequence version
Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prime sequence.
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                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; supplier: Giovannoni laborator; CLEC - Cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library" 149 c 143 g 228 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tomato callus, TAMU Lycopersicon esculentum cDNA clone similar to leucine-rich repeat protein (LRR), mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Lycopersicon
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="callus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="tomato callus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="25-40 days old"
/lab_host="XL1-Blue MRF/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="cLEC13C21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4081"
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74.3%;
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                                                                                                                                                                                                                                                                                                                                                                                   Score 317.2; DB 64;
Pred. No. 4.2e-77;
0; Mismatches 138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 339)

Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,
McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,
Retzel,E. and Somerville,C.

Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)

95148729
                                                                                                                                                                                                                                                                                                                                                                                                                       On May 5, 1977 Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
Michigan State University, Plant
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33800 Lan
                                                                                                                                                                                                                                                                                                                 Email: 22313tcn@ibm.cl.msu.edu
The sequence entry for this EST has been reverse complimented
is being submitted in the sense orientation.
Seq primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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517-353-9168
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Lambda-PRL2
                                               Inote-"Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRI2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The CDNA stages are plants as 3 but aerial tissue (stems).
inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA. "
75 c 66 g 89 t 5 others
                                                                                                                                                                                            /db_xref="taxon:3702"
/clone="179J11XP"
/clone_lib="Lambda-PRL2"
                                                                                                                                                                                                                                               organism="Arabidopsis/
strain="var columbia"
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179J11XP 3', mRNA
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Query Match Best Local Similarity

39.98;

Score 314.6; DB Pred. No. 2e-76;

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Sep 19, 1997 this sequence version
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Retzel, E. and Somerville, C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA cplant Physiol. 106, 1241-1255 (1994)
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31949 Lambda-PRL2
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Tel: 517-353-0854
Fax: 517-353-9168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSU-DOB-PRL, Michigan State University, Plant Biology Bldg., E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Michigan State University
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                                                                                                                                                                                                                                                                                                                il: 22313tcn@ibm.cl.msu.edu
primer: T7 dye primer.
    Location/Qualifiers
/clone_lib="Lambda-PRL2"
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: No
/note="Vector: lambda Zip-Lox; Site_1 Sal; Site_2: No
Lambda PRL2 is a CDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
                                                                                                                                                                                                      /db_xref="taxon:3702"
/clone="180C9T7"
                                                                                                                                                                                                                                               /organism="Arabidopsis
/strain="var columbia"
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Arabidopsis
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Raikhel, N., Somerville, S.,
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,S., Thomashow,
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180C9T7, mRJ
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                                                                                                                                                                        1 (bases 1 to 336)

Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,

McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,

Retzel,E. and Somerville,C.

Genes galore: a summary of methods for accessing results from

large-scale partial sequencing of anonymous Arabidopsis cDNA clones

plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                       sequence.
H37296
                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
                                                                                                            On May 8, 1995 this sequence version
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
                                                                                                                                                                                                                                                                                                                                                         H37296.1 GI:906795
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                                                                         Lansing,Mi
Tel: 517-353-0854
                                                                                                MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E
x: 517-353-008
x: 517-353-916
a11: 22313tcn@lbm.cl.msu.edu
aq primer: T7 dye primer:
Location/Qualifiers
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aacaacatccaaggaacta-taccttccgaacttgg 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACAACATNCACGGGGCTATTACCTTCCGAACTTGG
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                                Generation of ESTs from tomat
Unpublished (1999)
On Jul 8, 1999 this sequence
                                                                                                     1 (bases 1 to 646)
Alcala,J., Vrebalov,J., White,R., Matern,A.L.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L.,
Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksle
                                                                                                                                                                                               Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                             AW221939 646 bp mRNA EST 07-DEC-1999 EST298750 tomato fruit red ripe, TAMU Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                            clone cLEN6M3, mRNA sequence
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                   Contact: David Frisch
                                                                                       Giovannoni, J.
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                                                                                                                                                                               Lycopersicon.
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University
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86 c 69 g 89 t 13 others
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/strain="var columbia"
/db_xref="taxon:3702"
/clone="179J11T7"
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Genomics Institute
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Pred. No. 8.6e-
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, Ahn, S.,
ley, S.D. and
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RESULT 13
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hes 376;
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                                                                                                                                             aacggaccttttgctcacatt 580
                                                                                                                                                                                                                                                                                                                                                                         ctgtacaaccaaccttacagggatagttcccacttctttgggaaaattgaagtctctg 439
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                                                                                                                                                                                                                    atcccaagccttaaagttgttgatgtctcaagcaatgatttgtgtggaacaatcccaaca 559
                                                                                                                                                                                                                                                                       GTTTTCTTGCGTCTAAATGATAACAAGCTAACAGGACCAATCCCAAGAGAACTTACTAGC 565
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                                                                                                                                                                                                                                                                                                                                                                                                                               AATATTCAGGGAACCATCCCTAAGGAGCTCGGTAACTTGAAGAGCCTTATTAGTCTGGAT 445
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100 Jordan Hall, Clemson,
Tel: 864 656 4366
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Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
    AW350720
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/cultivar-"TA496"
/db_xref-"taxon:4081"
/clone_1lb-"tomato fruit red ripe, TAMU"
/tisue_type-"pericarp"
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/dev_stage="red ripe (7-20 days post-breaker)"
/note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/note-"vector: Glovannoni; Fruit were tagged at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe). 20 day fruit which showed external or internal signs of pathogenesis were discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
81 a 126 c 138 g 201 t
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hes 125;
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NNTGGTAACTCTAACCTATCTGGACATTTGGTACNNGAACTTGGGAAGCTGGAGCATCTA
                                                                                                                                    AGTCCCTGTACNNNNTCCACGTCNNNNGCAANCAGGACANNNNNGTCACTCGAGTGNAT 598
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363; Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae;
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On Nov 22, 1999 this sequence version replaced g1:6462107.

Contact: Vockin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)

Lewin, H. A., Director, Keck Center for Comparative and Functional
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Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Erpelding,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. and A Functional Genomics Program for Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134. For further information call: (800) 430-0030 or (314) 7-3222 FAX:(888)919-3324 or (314) 427-3324 or contact:clones@genomesystems.com or info@genome ystems.com web site:www.genomesystems.com seg primer: 5'-TTTTTTTTTTTTTTTTTTTTTT(A/C/G)-3'.
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Fax: (217) 333-4582
Email: 1-vodkin@uiuc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.genomesystems.com, and seq
Center for Comparative and Functional
University of Illinois,
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131 c 120 g 191 t 25 others
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The contig analysis to select unique genes was performed
by the laboratory of Ernest Retzel, Computational Biology
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/lab_host="XL10-Gold"
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/clone_lib="Gm-r1021"
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW221278 511 bp mRNA E.
EST297747 tomato fruit mature green, TAMU
CDNA clone cLEF13N13, mRNA sequence.
AW221278
AW221278 GI:6532962
                                                                                                                                                                                                                                                                Generation of ESTs from tomato fruit tissue Unpublished (1999) On Jul 7, 1999 this sequence version replace Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                               Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                    Clemson University Genomics Institute
                                                                                                                                                                                   Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                     Clemson University
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                                                                                                                                                                                                                            .00 Jordan
                                                                                                                                                                        sequence.
                                  /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEF13N13"
/clone_lib="tomato fruit mature green, TAMU"
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/tissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripen)
/lab_host="SOLR"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; cLEF - Fruit were tagged at the 1cm stage and harvested 3-5 days prior to ripening. Fruit were cut in
                                                                                                                                                        Location/Qualifiers
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Query Match
Best Local Similarity
Matches 370; Conserv
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Clemson
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                                                                                                                                                                                                                                                                                                                                                          AW030188 714 bp
EST273443 tomato cal
CLEC21C20, mRNA sequ
                                Unpublished (1999)
On Dec 20, 1995 this :
Contact: David Frisch
                                                                                                                     Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and
                                                                                                                                                                                                                                                                                                                                              AW030188
                                                                                                      Giovannoni, J
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                                                                                     Generation of ESTs from
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lemson University Genomics
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                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
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Pred. No. 1.7e-71;
0; Mismatches 122;
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Best Local Similarity 75.8%;
Matches 363; Conservative
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                                    atcccaagccttaaagttgttgatgtctcaagcaatgatttgtgtggaacaatcccaac 558
                                                                                                                                GTTTTCTTGCGTCTAAATGATAACAAGCTAACAGGACCAATCCCAAGAGAACTTACTAGC 653
                                                                                                                                                                        CTGTACAACAACAATATTTCGGGGGACAATTCCTACTTCACTTGGAAAACCTGAAAAACCTT 593
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/tlssue_type="callus"
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/lab_host="XL1-Blue MRF'"
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/clone="cleC21C20"
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/cultivar="TA496"
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Pred. No. 1.5e-70;
0; Mismatches 116; Indels 0;
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Search completed: June 23, 2000, 19:06:38 Job time: 27431 sec

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Perfect score:
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Listing first 45 summaries
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Maximum DB
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  June 24, 2000, 00:21:39; Search time 12463.9 Seconds
(without alignments)
-69.776 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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De, V.S., Schmidt, E.D., Van, H.G. a
PRODUCTION OF APOMICTIC SEED
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De, V.S. Schmidt, E.D., Van, H.G. a
PRODUCTION OF APOMICTIC SEED
Patent: WO 9743427-A 20-NOV-1997;
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De, V.S., Schmidt, E.D., Van, H.G. and
PRODUCTION OF APOMICTIC SEED
Patent: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
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Sequence
A67819
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1 (bases 1 to 981)

De, V.S., Schmidt, E.D., V

PRODUCTION OF APOMICTIC
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Pred. No. 6.7e-73;
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CIBA GEI
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Pred. No. 8.5e-72;
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DHYLQSWDPTLVNPCTWFHYTCNQDNRYTRYDLGNSNLSGHLAPELGKLEHLQYLELY
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HSRQSQAFKYYDYSSNDLGGTIPTNGPFFAHIPLQNFENNPRLEGPELLGLASYDTNCT
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Pred. No. 8.3e-66;
0; Mismatches 115
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2 (bases 1 to 4604)

Tornero, P., Mayda, E., Gomez, M.D., Canas, L., Conejero, V. and Vera, P. Characterization of LRP, a leucine-rich repeat (LRR) protein from tomato plants that is processed during pathogenesis
Plant, J. 10 (2), 315-330 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Asteridae; Solananae; Solanales; Solanaceae; Solanum; Potatoe;
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                                                                         /translation="meavekroslelkimgilavvlavavavkgnsegdalvalrrsi
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                                                                                                                                                                                                                                                     113. .4355
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2381. .2452
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4283. .4355)
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Embryophyta; Urridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyliophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Sequence 32 from Patent
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(bases 1 to 2089), V.S., Schmidt, E.D.,
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/db_xref="taxon:3702"
/clone="SERK GENE CDNA"
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/codon_start=1
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/db_xref="GI:4756650"
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Schmidt, E.D., Guzzo, F., Toonen, M.A. and de Vries, S.C. A leucine-rich repeat containing receptor-like kinase marks somatic plant cells competent to form embryos Development 124 (10), 2049-2062 (1997)
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ilarity 56.1%;
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/protein_id="AAB61708.1"
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ReslrelovatDTFSTILGRGGFGKYYKGRLADGSLVAVKRLKEERTPGGELOFGTEV
EMISWAVHRULLELGFCMTFTELLVTYMANGSVASCLREROPSEPFLDWFTRKRI
ALGARGISYLHDGDFKIHRDYKAANILLDEFERAVGDDGCLARLANDDDVMLLDWV
KSLLKEKKLEMLVDPDLENNYIDTEVEGLIQVALLCTGGSPAFDLARLANDDDVMLLDWV
KSLLKEKKLEMLVDPDLENNYIDTEVEGLIQVALLCTGGSPAFDLARLANDDDVMLLEGDG
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/db_xref="taxon:4039"
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Pred. No. 3.8e-12;
0; Mismatches 141;
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                                                                                                                                                                                                                                                                                                                                                                                                                           agagaactcacagttatttcaagccttaaagttgttgatgtctcagggaatgatttgtgt 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGCTTACAAGGCTAAGATTCTTGCGTCTCAACAACAACAGCCTCTCTGGTCCAATTCCA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amattgaagtcacttgttttttttgcggcttaacgaamaccgattgaccggtcctattcct 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ctaatcagtitggatctgtacaacaacaatctcaccgggaaaatcccatcttctttggga 438
                                                                                                                                                                                                                TTGAATTTATGTGGACCCGTA 498
                                                                                                                                                                                                                                                                                                        GGACCAGTACCGGATAATGGCTCATTTTCTTTGTTTACACCTATCAGTTTTGCCAATAAT 477
                                                                                                                                                                                                                                                                                                                                            ggaacaattccagtagaaggaccttttgaacacattcctatgcaaaactttgagaacaac 618
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
1 (bases 1 to 1815)
De.V.S., Schmidt, E.D., Van, H.G. and Hecht, V.F.
PRODUCTION OF APOMICTIC SEED
Patent: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
A67797
                             SBU62279 936 bp mRNA PLN 09-DEC-1996 Sorghum bicolor leucine-rich repeat-containing extracellular glycoprotein mRNA, complete cds. U62279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAB42241.1"
//protein_id="CAB42241.1"
//protein_id="CAB42241.1"
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//translation="MNRNSINILNYMQFTDAYLDKYGYLMTLELYSNNISGPIPSDLG
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SNNRLSGPVDDNGSFSLFTPISFANNLNLCGPVTGRPCPGSPPFSPPPFIPPSITVOP
PGQNRPTGALAGGTVAAGAALLFAAPAMAFAWMFRRKFRERETPDVPAREDEPWHLGQLK
RFSLRELQVATDTFSTILGRGFGKVYKGTLADGSLYAVKRLKEERTPGGELOPQTIEV
EMISMAVHRULLRLGGFCMTPTERLLVVFYMANGSVASCLRERQPSEPPLMPTTRA
RESARGLSYLHDHCDPKIIHRDVKAANILLDEEFEAVVGDEGLARLMDYKDTHVTTA
VRGTLGYIAAFFLSTGKSSEKTDVFGYGIMLLEIJTGGRAFDLARLANDDVMLLDMV
KSLLKEKLEMIVDPDLENNY IDTEVEGUIQVALLCTGGSFWERFKMSEVVRMLEGDG
LAEKWDEWGKVEVIHQDVELAPHRTSEWILDSTDNLHAFELSGPR"
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/db_xref="taxon:4039"
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Pred. No. 3.7e-12;
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Matches 250;
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acaccatcaagtcactcgtctggatttggggaattcaaacttatctggacatctagtacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                               tcagagttgggatccaactcttgttaatccttgtacttggtttcatgtcacttgtaatca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctccgaaggggacgctcttcacgcggcttcgccggagcttatcagatccagacaatgttgt 74
                                                                    ---GGATCTCTGGGACAACCTTCTTACCGGCGAAATCCCAACTACGCTTGGTTCTGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACTGAAGGTGACATACTGTACAAGCAAAGGTTGGCATGGGAGGACCCCAAACAACGTGCT 142
                                                                                                 tagtgaactctacaaaaacgagattcaaggaactataccttctgagcttggaaatctgaa
                                                                                                                                                               TTCGATTCCAGAAACACTAGGCAACCTGACTAATCTCATCAGCTT-------
                                                                                                                                                                                                        tgattatctgaaaacatttacattatcagtcacacatataacattttgctttgagtcata
                                                                                                                                                                                                                                                    AGATCTTGCAGAAATTCAGAACCTCCAGTACATCGAGCTGTATGGCAACGGCTTGAACGG
                                                                                                                                                                                                                                                                                                tgaacttgggaagcttgaacatttacaatatctgtatggaatcatcactcttttgccttt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol.
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Poaceae; Sorghum.
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euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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232 c 207 g 250 t
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LTSLLESKLQENSLSGAIPASLGNIKALQFSKLNDNMLTGTVPSKSFPLSTFGNLTEL
NTDRNNLDGTRTSSGLRVTAIIQDALKTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAC49559.1"
/db_xref="G1:1710114"
/db_xref="G1:1710114"
/theanslation="MAPGPAAAGFLTGLLALATFASCNTEGDILYKORLAWEDPNNVL
/translation="MAPGPAAAGFLTGLLALATFASCNTEGDILYKORLAWEDPNNVL
OSWNSTLANPCTWFHVTCNNNNFVIRVDLGNAGISGPLLPDLAEIQNLQYIELYGNGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="protein-protein ligand binding"
/note="leucine-rich repeat-containing extracellular
glycoprotein; contains six N-glycosylation sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone="SLRR"
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Best Local Similarity
Matches 142; Conserv
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                                                                                                                                                                                                                                           30536 TTGATTTGGCCATCGGAAAGCTCAGTGGTGAGATTCCGTCAGAGCTTGGGAAGCTCAAGT
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                                   cagttatttcaagccttaaagttgttgatgtctcagggaatgatttgtgtggaacaattc 568
                                                                                                                                                      cacttgtttttttgcggcttaacgaaaaccgattgaccggtcctattcctagagaactca
                                                                                                                                                                                                                                                                                     tggatctgtacaacaatctcaccgggaaaattcccatcttttgggaaaattgaagt 448
                                                                                                                                                                                                                                                                                                                                                                                                           aaaacgagattcaaggaactataccttctgagcttggaaatctgaagagtctaatcagtt 388
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GAAGCATTACCACGCTAAAGGTTCTTGATTTCTCCGATAATGCGTTAACCGGCGAGATTC
                                                                                                                     CACTCGAGACGCTTCTCCTGTACGAGAATAACTTCACCGGAACAATTCCAAGAGAGATAG
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For more information about this sequence or the ESSAII project, see MIPS http://websvr.mips.biochem.mpg.de/proj/thal/. Order of segments is not known; 800 n's separate segments.

* NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be
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Arabidopsis thaliana clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis.
1 (bases 1 to 43277)
Lennard, M., Quail, M., Harris, B., Rajandream, M.A.
Direct Submission
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/variety="Columbia"
/db_xref="taxon:3702"
/clone=""D5F17"
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T5F17, *** SEQUENCING IN PROGRESS ***,
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                                                                                                                                            Query Match 8.7%;
Best Local Similarity 57.0%;
Matches 142; Conservative
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                                                          323 totacaaaaacgagattcaaggaactatacottotgagottggaaatotgaagagtotaa 382
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elicitor-Inducible receptor-like protein EIR.
Nicotiana tabacum mRNA.
Nicotiana tabacum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Solanaceae;
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Location/Qualifiers
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Isolation of the gene for EIR, an elicitor-inducible receptor-like protein, from tobacco by Differential Display Unpublished (199)

(bases 1 to 2786)

Takemoto, D. and Kawakita, K.

Direct Submission
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/product="elicitor-inducible receptor-like protein
/protein_ic=1"BAA88636.1"
/db_xref="GI:6635236"
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/db_xref="taxon:4097"
                                                                                                                                               0;
                                                                                                                                            Score 77.8; DB 7;
Pred. No. 3.8e-08;
0; Mismatches 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tasaski@abr.affrc.go.jp, URL:http://www.dna.affrc.go.jp:82/, Tel:81-298-38-7441, Fax:81-298-38-7468)
The orientation of the sequence is from T7 to SP6 of the PAC clone. Genes were predicted from the integrated results of the following:GENSCANI.0, BLASTNZ.0, BLASTNZ.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against the non-redundant database NRP (PIR, SWISSPROT, GENPEPP, PDB) from MAFF DNA bank and the cDNA sequence database at RGP. Protein similarities of the cording regions were searched against NRP with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession
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Direct Submission
Submitted (30-NOV-1999) to the DDBJ/EMBL/GenBank databases. Takuji
                                                                                                                                                                                                                                                                                                                                                                                                                               no. and RGP clone ID.

Detailed information on assemble quality together with annotation of this entry at http://www.dna.affrc.go.jp:82/genomicdata/GenomeFi
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Oryza sativa
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sativa genomic DNA,
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/db_xref="taxon:4530"
/chromosome="1"
/clone="p0003H10"
                 /translation-"MGEFNQRRLYQVWQGSNKFLCGGRLIFGFDAGSLFLSTVLIVAP
LVGLCCQCITKMNSISSEKQVLGLPVLIATIYLGLADLAFLLMTSSRDFGIVFRNARP
                                                                     /protein_id="BAA87822.1"
/db_xref="GI:6498419"
                                                                                                                                     /note-"Similar to Arabidopsis
BAC clone F22K18 (AL035356)"
                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
PESCGGGDEEGVAGDVTTPSAEWVTAASPHLRLPRSKDVVVNGCVVKVKYCDTCLLYR
                                                                                                                   /codon_start=
                                                                                                                                                                                                               oin(2901.
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                                                                                                                                                                                             .5509)
                                                                                                                                                                                                               .2951,3129. .3317,3521. .3850,4405. .4638,
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                                                                                                                                                                    thaliana DNA chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome
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/note="ESTS AU081256(C53656), AU081257(C53656),
AU032236(R3784), AU081351(E61905), AU031587(E61905),
AU031236(R3784) correspond to a region of the predicted gene.; Similar to alien-like protein. (AC005623)"
/codon_start=1
/protein_id="BAA87824.1"
/db_xref="G::6498421"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAAKPGTPKKRGKTEIQETLLTPRFYTTDEDEMERLENAEINKQLNQEEFDALLQEEK
TDYNQTHFVRNPEFKAAADKMGGPLROLIFVEFLERSCTVAEFSGFILIYKELGRRLKKTN
PVVAEIFSLMSRDEARHAGFLNKGLSDFNLALDLGFLIKARKYTFFKPKFIFVAFUS
EKIGYWRYITLIFRHLKANDEYQYYEJEKYFENNCQDENRHGDFFSALLKAQPQFLNDW
KAKLMSRFFCLSYYVTMYLNDCQRTTFYEGIGLDTKEFDMHVIIETNRTTARIFPAVL
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                           PHPRIMGIIREGGGKHMABROWADAATDFFEAFKUNDEAGNERRIQCLKYLVLANMI
MESEVNPEDGCEAKPYKNDPE ILAMTNLIAAATQKUDIKE
NYIEDLLKNIRFQVLLKLIKPYTRIR, IPFISOKWCMKIISNMELWYILVEHGTLVYI
RAIIGSCKKYSLKLDLELSCAOTRVOLKSCALNRADPMLFLTEVNLLSYSVODALSSI
VLSMFCMELNFPEKDVEQLLVSLILDNRIGGHLDVNKILLERGENEIPSETTIASH
EHLPNGVQOSWYRELAGCLGCTALGTCLHVLMWMLGFCPELMLSANSNPSETTIASH
ARNFWFCWHCRISKFWYGRENVWFRVKYAPGIRHTANIVPLPSSDSVANQSLSNQNEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MedygfeySddepeeQdvDIENQYYNSKGMVETDpegalagfdq
VVRMEDEKAEMGFKALKQTVKLYKLGKYKEMMDAYREMLTYLKUKYRWYSEKCINU
IMDFYSGSASONFSLLOEFYQTTLKALEEKKERKEMFKINLKLCKIWFDMOEYGRMSK
ILKELHKSCQREDGSDDQKKGTQLLEVYAIEIQMYTETKNNKKLKELYTKALSIKSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(13373..13457,15836..15914,17237..17477,17560..1
17726..17860,18400..18587,18681..18749,18826..18916,
19028..19162,19323..19379,19349..19441,19450..19509,
19523..19585,19589..19701,19800..19941,20057..20294,
21399..21586)
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LTGGVKEKVDLEMGRNGGIIPAILRGLDYDEMEKNDVSVHIKDRGAAPAAPDPFMAGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                AAELRHVMTNLGEKLIDEEVEEMIREADVDGDGQINYDEFVKVMMAK"

complement(join(24778. .24897,25615. .257.22,25808. .25893,

26090. .26177,26435. .26638,27519. .27581,27708. .27778,

28329. .28389,28512. .28552,29058. .29225,30476. .31136))

/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(22475 . 22550,23332 . 23705)
/note-"ESTS AUG30013(E50493), AUG81341(E50493) correspond
to a region of the predicted gene.; Similar to O.sativa
gene encoding calmodulin. (Z12828)"
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/db_xref="GI:6498420"
/translation="MASSAMELSLLNPAAMRGLSAAKPRVVSSRRIVRFRVASSAAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KESPFLSYTTDQQALNLQREHTTLSDNYINLSEGSYRPLAPSSHLGHPYYT1FYVDDN
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TEAELQDMINEVDADGNGTIDFPEFLNLMARKMKDIDSEEELKEAFRVFDKDQNGFIS
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ISGFGVLVYQLAIYPLLAKYVGPIKPFRYAAVLSILLLSTYPFMANLYGLELKVLINI
                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=
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/db_xref="GI:6498422"
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SGS
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GIPYLNFFYIWVVCLCSFPRRYRPAKKICDFSVKAMAHGHRR"
join (40347. 40358, 40468. 40680)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MSRGRGRAPATACGSVRCYABEVAPEQEDSARYALLILIRLRDSP
AATAPPKLARRIRDHGVPLLERDEDLISVGPTLD"
join(48412. 48822,49072. 49179,49283. 49438,49876. .5009
50202. .50411,50488. .50625,50842. .50943,51105. .51170,
51274. .51358,51454. .51551)
/note="Similar to Arabidopsis thaliana chromosome II BAC
727416 sequence; hypothetical protein. (AC005496)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(52616. .52685,53228. .53299,53395. .53466,
53657. .53800,54663. .54734,56026. .56334))
/note="ESTS C97644(C60871),AU081265(C60871) correspond to
a region of the predicted gene.; Similar to L.esculentum
LRP gene. (X95269)"
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complement(join(42025. .42083,43481. .43661))
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/db_xref="GI:6498424"
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                   /translation="MAAAWSPALAAVLLAAAVASASNSEGDALYALRRALADPRGVLQ
SWDPTLVNPCTWFHVTCDRAGRVTRLDLGNSNLSGHLAPELGHLEHLQYLELYKNNIQ
GTIPAELGSLKNLISLDLYNNNITGTIPKELGKLSSLVFLRLNDNSLNGPIPRDLAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSVFYSFGSLGVFWFSTWASKAYSSPLEDPGISAEEKKLITSQTTGGEPVKEIFWGLI
LSKPPVWALIVSHFCHNWGTFILLTWMPTYYNQVLKFNLTESGLFCVLFWLTMAVSAN
FGGWIADTLVSRGLSVTTVRKIMQSIGFLGPAFFLTQLSHIDSPAMAVLCMACSQGTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRALRGTDVRSNTSSSSSRKGRHDDARHDGGYGDDGDAGALLASVRRLLLSGSAQDD
AAEGEAEEDEGGGFFKRWAIVFLCFSAFLLCNMDRVNMSIAILPMSAEFGWNPQTVGL
IQSSFFWGYLLTQIAGGIWADTVGGKTVLGFGVIWWSIATALTPFAAKLGLPFLLVTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MAAGDKAGGDDAAAAAPLLVPAAAGRRRRCPGCRTKERCEAHPG
| PYLINFYLWIVCICASAVNRVEATEVMPTSTSVS"
| Join(47081. .47084.47194. .47313.47469. .47584)
| /note="hypothetical protein"
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/db_xref="GI:6498426"
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                                                                                                                                                                                                                                                                                                                                 SSLKVIDVSNNDLCGTIPTSGPFEHIPLNNFDKNPRLEGPELQGLATYDTNC'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFSQSGLYSNHQDIGPRYAGVLLGLSNTAGVLAGVFGTAATGYILQHGSWDDVFKVSV
VLYLVGTLVWNLFSTGEKIID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFMGVGEGVAMPAMNNILSKWVPVSERSRSLALVYSGMYLGSVTGLAFSPLLIHNFGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAA87831.1"
/db_xref="GI:6498428"
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/db_xref="GI:6498427"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAA87828
/db_xref="GI:6498425"
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/translation="mrrsrartdlraagrataelrrrgrrsrgrgqeeyigtasiggg
egstsdewegrggegrgaaavrpageerrrhraetkigisilvggrgaphrqsgghg
eggrdeegelmlvggalrpeeeeeeeghgrrrgrrgeerrvcerereer"
                                                                                                                                                    KTGTSSLTGSVPSKDRSRNRPGVNLADH" complement(join(63689. .63842,63844.
                                                                                                                                                                                                                       /protein_id="BAA87833.1"
/db_xref="GI:6498430"
                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAA87832.1"
/db_xref="GI:6498429"
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                                                                                                                                                                                                                                                                                     /note="hypothetical protein"
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                                                            /protein_id="BAA87834.1"
/db_xref="GI:6498431"
                                                                                                                               /note-"hypothetical protein"
                                                                                                                                                                                               translation="MKLLKVDHPRSHHTVFLYASLTSIALYTSLTIIVEKTGLAVQPE"
                                                                                                          /codon_start=)
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AUTHORS
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Matches 141;
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53820 TTTTTGAAAAATTGTTACAGAGAGCTGTACAAAAACAATATTCAGGGCACTATCCCAGCT 53761
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                                                    CAGTICITGATCTTTCCAACAACAAATTCTCAGGTCAAATTCCTGCCTTGTTCTCCAAGC
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tgaagtcacttgtttttttgcggcttaacgaaaaccgattgaccggtcctattcctagag 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-JAN 1998) to the DDBJ/EMBL/GenBank databases. Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory of Gene Structure 2: 1532-3, Yana, Kisarazu, Chiba 292, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopleuphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Local Similarity 54.7%;
hes 146; Conservative
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12 1 (bases 1 to 3176)

13 Mitsukawa, N. and Robaato, E.U.

14 EXEMPTION OF PROTEIN CONTROLLING MORPHOGENESIS OF PLANT

15 PAtent: JP 197056382-A 1 04-MAR-1997;

16 CHIKYU KANKYO SANGYO GIJUTSU KENKYU KIKO, MITSUI GYOSAI SHOKUBUTSU

17 PATADIOPSIS thaliana (thale cress)

18 PN JP 1997056382-A/1

19 PN JP 1997056382-A/1

10 04-MAR-1997

10 14-MAR-1997

11 MITSUKAWA NORIHIRO, ROBAATO EFU UITSUTEIA

11 CC 12015/09, A0145/00, C12N5/10;

12 CC topology: Linear;

13 Source (Organism='Arabidopsis thaliana' FT

11 Source (Organism='Arabidopsis thaliana' FT

11 Control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of 
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                        tgatttgtgtggaacaattccagtaga 575
TGATATCTCTGGCCCAATTCCAGAAGA 1531
                                                                                                         TGTAGTTCCAGGCGACTTTGGAAATCTAAGAAGCATCATGGAAATAGATCTTTCAAATAA
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Arabidopsis thaliana cDNA encoding a protein involved in
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O. sativa Xa21 gen
Tomato Cf-9 CDNA.
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Tomato Cf-9 gene.
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O. longistaminta X
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D 20-NOV-1997.
D 20-NOV-1997.
F 13-MAY-1996; GB-010044.

R 14-MAY-1996; GB-010044.

PA (NOVS) NOVARTIS AG.

PI De Vries SC, Hecht VEG, Schmidt EDL, Van Holst GJ;

PR WF1; 98-086529/08.

PR P-PSDB; W47021.

PR P-PSDB; W47021.

PT Production of apomictic seeds - useful in plant breedi
PT Production 98; Pages 83-84; 123pp; English.

CC The sequence is that of an EST clone showing high home
CC SERK LARR (Leucine-rich repeat) sequences.

CC Carmence 894 BP; 270 A; 163 C; 176 G; 2
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Best Local S
Matches 894
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03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST clone.
receptor kinase; apomixis; apomictic; seeds; production;
plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
Location/Qualifiers
CDS
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                                              tgotttgagtcatatagtgaactctacaaaaaacgagattcaaggaactataccttctgag
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T42425
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T78868
T78868
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T78867
V26098
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Best Local Similarity 72.8%;
Matches 538; Conservative
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03-AUG-1998 (first entry)
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous Es
receptor kinase; apomixis; apomictic; seeds
plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
Key
CDS
2..664
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20-N0V-1997; E02443.
13-MAY-1996; GB-01044.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, S
WPF; 98-08529/08.
P-PSDB; W47020.
                                                                                              Production of apomictic seeds - useful in plant breeding Claim 28; Payes 79-80; 132pp; English.
The sequence is that of an EST clone showing high homolog SERK LRR (leucine-rich repeat) sequences.

Sequence 788 BP; 234 A; 191 C; 156 G; 207
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tcagagttgggatccaactcttgttaatccttgtacttggtttcatgtcacttgtaatca
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Pred. No. 3.7e-88;
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W09743427-A1.

20-NOV-1997.

13-MAY-1997. E02443.

14-MAY-1996. GB-010044.

(NOVS ) NOVARTIS AG.

De Vries SC, Hecht VFG, Schmidt EDL, Van Holst
WPI: 98-086529/08.

P-PSDB; W47022.

Production of apomictic seeds - useful in plant
Claim 28; Pages 86-88; 123pp; English.
The sequence is that of an EST clone showing hi
SERK LRR (leucine-rich repeat) sequences.
                                                                                                                                                 V06590 standard; cDNA to mRNA; 1063 BP. V06590; 03-AUG-1998 (first entry) Arabidopsis thaliana SERK LRR homologous receptor kinase; apomixis; apomictic; see plant breeding; leucine-rich repeat; ss. Arabidopsis thaliana.
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Best Local Similarity
Matches 538; Conserv
                 V06587 standard; cDNA to mRNA; 981 BP.
V06587;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous ES receptor kinase; apomixis; apomictic; seeds plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
Key
CDS
104. .760
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                                                                                                                                                            CTGAAAAATTGGCAAAACCTGAAAATGAAGAATTGGGGGGGTGACCTTGTAAGAACACTT
                                                                                                                                                                                             CAACCCGAGGTTGGAGGGACCGGAATTACTCGGTCTTGCAAGCTACGACACTAACTGCAC
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Pred. No. 4.1e-88;
0; Mismatches 11(
high homology
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Best Local Similarity
Matches 535; Conserv
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20-N0V-1997, E02443
13-MAY-1996; GB-010044.
[NOVS] NOVARTIS AG.
[NOVS] NOVARTIS AG.
De VI16S SC, Hecht VFG, S
WFI; 98-08559/08.
P-PSDB; W47019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Production of apomictic seeds - useful in plant by Claim 28; Pages 75-77; 133pp; English.
The sequence is that of an EST clone showing high SERK LRR (leucine-rich repeat) sequences.
Sequence 981 BP; 286 A; 236 C; 180 G;
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                                                                                         tagtgaactctacaaaaacgagattcaaggaactataccttctgagctttggaaatctgaa
---AGAGCTCTACAAAAACAACATCCAAGGAACTATACCTTCCGAACTTGGAAATCTGAA
                                                                    ttaaaaagaagttgaagaacctataaagaagaa-tgttaggtgaccttgtaagaactctg
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                                         taccaagtgtttgtaaatc
                                                                                                                                                           CCCTAGAGCACTCACGGCAATCCCAAGCCTTAAAGTTGTTGACGTCTCAAGCAATGATTT
                                                                                                                                                                                             GGGAAAATTGAAGTCTCTGGTCTTTTTACGGCTTAATGACAACCGATTGACCGGTCCAAT
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                                                         CTGAAACAACTGGCAAAACCTGAAAATGAAGAATTGGGGGGGTGACCTTGTAAGAACACTT
                                                                                                                                                                                                                                                                                                                                 TGAGCTTGGGAAGCTTGAACATTTACAGTATCT---
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ilarity 72.4%;
Conservative
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Pred. No. 7.8e
0; Mismatches
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Best Local S
Matches 532
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20-N0V-1997.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, S
WPI; 98-086529/08.
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Key
CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana SERK LRR homologous EST clone. receptor kinase; apomixis; apomictic; seeds; production; embryos; plant breeding; leucine-rich repeat; ss.
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V06586;
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acaacctgagattggagggaccagaactactaggtcttgcgagctatgacaccaattgca
                                                                      TGTGTGGGACAATCCCAACAAACGGACCCTTTGCTCACATTCCTTTACAGAACTTTGAGA
                                                                                                  tgtgtggaacaattccagtagaaggaccttttgaacacattcctatgcaaaactttgaga
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nilarity 71.9%;
Conservative
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Pred. No. 9.2e-80;
0; Mismatches 115
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Production of apomictic seeds.

Claim 27; Pages 91-95; 123pp; English.

Claim 27; Pages 91-95; 123pp; English.

Claim 27; Pages 91-95; 123pp; English.

Claim 27; Pages 91-95; 123pp; English.

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Claim 27; Pages 91-95; 123pp; English.

Claim 27; Pages 91-95; 123pp; English.

Claim 27; Pages 91-95; 123pp; English.

Claim 27; Pages 91-95; 123pp; English
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Best Local S
Matches 257
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Arabidopsis thaliana SERK greceptor kinase; apomixis;
plant breeding; ds.
Arabidopsis thaliana.
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20-N0V-1997; E02443.
13-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, 198-086529/08.
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cttgggaagcttgaacatttacaatatctgtatggaatcatcactcttttgccttttgat
                                                                    catcaagtcactcgtctggatttggggaattcaaaacttatctggacatctagtacctgaa 198
                                             AACAGTGTCATAAGAGTTGATTTGGGGAATGCAGAGTTATCTGGCCATTTAGTTCCAGAG
                                                                                                                                 AGCTGGGATCCTACGCTAGTGAATCCTTGCACATGGTTCCATGTCACTTGCAACAACGAG 398
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257; Conserv
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195. .2072
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53.5%;
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.2e-19;
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                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                        plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated.

Apomixis allows plant breeders to develop cultivars with seed and forage quality and maturity.

Sequence 1814 BP; 530 A; 354 C; 415 G; 515 T;
                                                               Query Match
Best Local s
Matches 180
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20-NOV-1997.
13-MAY-1997; E02443.
14-MAY-1996; GB-01004
                                                                                                                                                                                                                                                                                                                                                                       Production of apomictic seeds - useful in plant breeding Claim 21; Pages 47-51; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising; (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing the transformed material into plants or carpel-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Daucus carota SERK gene.
receptor Kinase; apomixis; apomictic; seeds; production; embryos; plant breeding; ss.
Daucus carota.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NOVS ) NOVARTIS AG.
De Vries SC, Hecht VFG, Schmidt EDL, Van
WPI; 98-086529/08.
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                   gaactctacaaaaacgagattcaaaggaactataccttctgagcttggaaatctgaagagt 378
GAGCTTTACAGCAATAACATAAGTGGACCAATTCCTAGTGATCTTGGGAATCTGACAAAT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                              Similarity
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/product=
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                                                                              10.7%;
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Pred. No. 1.5e-16;
0; Mismatches 141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding plant morphogenesis regulatory protein - useful to yield plants with short stems or altered inflorescence Claim 1; Pages 6-10; 17pp; Japanese.

The present sequence encodes an Arabidopsis thaliana plant morphogenesis regulatory protein (MRP), which can be used to yiel a plant with, e.g. short stems or altered inflorescence. The MRP cacts on a plant at a specific site for a specific period, and can therefore be used to regulate extraneous gene expression in a plant. The MRP's cDNA or genomic DNA can be used to transform a plant to increase its MRP expression, and therefore control the form (particularly stem length) of the plant.

Sequence 3176 BP; 927 A; 654 C; 659 G; 936 T;
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 54.7
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     762124 standard; cDNA to mRNA; 3176 BP.
762124;
10-JUN-1997 (first entry)
10-JUN-1997 (first entry)
Arabidopsis thaliana plant morphogenesis regulatory protein cDNA.
Plant; morphogenesis; regulation; short; stem; alteration;
inflorescence; extraneous; gene; expression; transformation;
increase; control; form; length; ds.
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04-MAR-1997.
04-MAR-1997.
24-AUG-1995; 216187.
24-AUG-1995; JF-216187.
24-AUG-1995; JF-216187.
0MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
(CHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYU
WPI; 97-206629/19.
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TTCCCTTGGTGATTTGGAGCATCTTCTCAAGATGAACTTGAGTAGAAATCATATAACTGG
                                                                                                                  TATCGGTAACTTAGATACATTGGATCTTTCCAACAACAAGATAAATGGAATCATTCCTTC
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                                                   trotttgggaaaattgaagtcacttgtttttttgcggcttaacgaaaaccgattgaccgg
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/note= "plant morphogenesis regulatory protein"
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; Pred. No. 1.6e
0; Mismatches
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L.6e-10;
hes 121;
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                 Production of apomictic seeds - useful in plant breeding Claim 26; Pages 64-67; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V06585 stand
V06585;
03-AUG-1998
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Key
CDS
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WPI; 98-086529/08.
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) NOVARTIS AG.
les SC, Hecht VFG, Schmidt EDL, Van Holst
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           plant.
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GB-010044.
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3731. .3802
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/*tag= f
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/*tag= c
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/*tag= 1
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            Apomixis
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          true-breeding,
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Best Loc
Matches
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Sequence 4081 BP; 1120 A; 770 C; 785 G; 1406 T;
T06307 is a tomato pathogen resisitance gene Cf-2.2 partial cDNA clone. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagales of plants) containing such constructs. Cf-2.2 imparts resistance to the disease caused by the leaf mould fungal pathogen Cladosporium fulvum. C.fulvum containing avirulence (Avr) genes that confer recognition by plants containing Cf-genes, leading to the activation of host defence mechanisms to attack the disease.

Sequence 3573 BP; 1032 A; 654 C; 664 G; 1223 T;
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                                                                                                                                                   P-PSDB; R85299.
Increasing plant pathogen resistance by induction may lead to acquired resistance to a broad range c claim 9; Page 85-87; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            Partial tomato pathogen pathogen ren'
                                                                                                                                                                                                               (GATS-) GATSBY CHARITABLE Hammond-Kosack KE, Jones WPI; 96-010949/01.
                                                                                                                                                                                                                                                                                                                                                     Lycopersicon esculentum WO9531564-A2.
                                                                                                                                                                                                                                                                                                                                                                               Leaf
                                                                                                                                                                                                                                                                                                                                                                                               Partial tomato pathogen resistance gene Cf-2.2 cDNA clone.
Pathogen resisitant; Cf-2.2; tomato; C.fulvum; Avr 4; Avr 9; fungal;
                                                                                                                                                                                                                                                           31-MAR-1995; GB-006658.
07-APR-1995; GB-007232.
                                                                                                                                                                                                                                                                                       23-NOV-1995.
11-MAY-1995; G01075.
11-MAY-1994; GB-009394.
23-DEC-1994; WO-G02812.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mould; variegation; ss.
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Pred.
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Best Local Similarity

54.0%;

Pred. No.

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                              11-MAY-1995; G01075.

11-MAY-1994; GB-009394.

23-DEC-1994; WO-G02812.

31-MAR-1995; GB-006658.

07-APR-1995; GB-007232.
                                               Increasing plant pathogen resistance by induction of variegation—may lead to acquired resistance to a broad range of pathogens.

Claim 9; Page 80-83; 131pp; English.

T06306 is the tomato pathogen resistance gene Cf-2.1. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagules of plants) containing such constructs. Cf-2.1 imparts resistance to the disease caused by the leaf mould fungal pathogen Cladosporium fulum.

C. fulvum contains avirulence (Avr) genes that confer recognition by plants containing Cf-genes, leading to the activation of host defence mechanisms to attack the disease.

Sequence 6471 BP; 2073 A; 1106 C; 1122 G; 2170 T;
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Hammond-Kosack KE, Jones DA, WPI; 96-010949/01.
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5015. .
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1677. .1745
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1746. .5011
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1677. .5014
/*tag= b
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54.
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 . 48;
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Score 66.4;
Pred. No. 1
                                                                                                                                                                                                                                                     Jones JDG;
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C.fulvum;
 DB 1;
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           Length 6471;
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Local Similarity hes 138; Conserv

309 gtcatatagtgaactctacaaaaacgagattcaaggaactataccttctgagcttggaaa 368

125;

Indels

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Gaps

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                                                                                 PT Tomato gene Cf-5, confers resistance to Cladosporium fulvum - useful production of transgenic plants resistant to pathogens e.g. for production of transgenic plants resistant to pathogens e.g. production of transgenic plants resistant to pathogens e.g. for production of transgenic plants. The polynucleotide of the invention, which cfic can be produced by incorporating the gene variants, which offer cresistance against the pathogen Cladosporium fulvum-5. Transgenic plants can be produced by incorporating the gene into plant cells and coffspring can also be subsequently produced. Expression of the gene in complementary to the gene or fragments with sequences complementary to the gene or fragments of it, are useful in anti-sense techniques to reduce gene expression. The nucleic acids/polynucleotides care useful as hybridisation probes to identify other genesty resistance in potentions. Homologies between Cf-5 and Cf-9 may be used to identify continues of this class.

So Sequence 3541 BP; il23 A; 630 C; 612 G; 1176 T;
 Query Match
Best Local S
Matches 138
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20-NOV-1997.
08-MAY-1997; (
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V14522;
20-MAY-1998 (first entry)
CF-5 pathogen resistance gene clone Hcr2-5B gene.
Tomato; CF-5 pathogen resistance gene; Cladosporium tomato leaf mould; Phytophthora resistance; ss.
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Key Location/Quali
CDS 603. .3002
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09-MAY-1996; GB-009681.
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ilarity 52.5%;
Conservative
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Score 63; DB 1;
Pred. No. le-07;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor kinase; a plant breeding; ds Daucus carota. Key CDS
                                                                           14-MAY-1996; GB-010044.

(NOVS) NOVARTIS AG.

De Vries SC, Hecht VFG, S

WPI; 98-086529/08.

P-PSDB; W47013.
P-PSDB; W47013.

P-PSDB; W47013.

Production of apomictic seeds - useiu....

Claim 21; Pages 40-46; 123pp; English.

Claim 21; Pages 40-46; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase.

It may be used as part of a method of producing apomictic seeds of morising: (a) transforming plant material with a nucleotide composition; (a) transforming plant material with a cell or
                                                                                                                   WO9743427-A1.
20-NOV-1997.
13-MAY-1997; E
14-MAY-1996; G
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Apomixis allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.

Seed and forage quality and maturity.
This sequence is an example of the polynucleotide of the invention, and is able to confer pathogen resistance on a plant. It is one of two tomato CF-5 gene variants, which offer resistance against the pathogen resistance against the pathogen resistance against the pathogen confer pathogen plants can be produced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced by incorporating conferenced conferenced by incorporating conferenced conferenced conferenced complete conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferenced conferen
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Best Local
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Tomato; CF-5 pathogen resistance gene; Cladosporium fulvum-5;
tomato leaf mould; Phytophthora resistance; ss.
Lycopersicon pimpinellifolium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V14518 standard;
V14518;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tomato gene Cf-5, confers resistance to Crados for production of transgenic plants resistant tomato leaf mould C. fulvum in tomatoes Claim 3; Fig la; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dixon MS, Hatzixanthis K, Jones WPI; 98-008895/01.
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Promato gene Cf-5, confers resistance to Cladosporium fulvum - useful production of transgenic plants resistant to pathogens e.g.

Production of transgenic plants resistant to pathogens e.g.

Production of transgenic plants resistant to pathogens e.g.

Claim 6; Fig 1b; 75pp; English.

CC This sequence is an example of the polynucleotide of the invention, and confer pathogen resistance on a plant. It is one of two tomato confer pathogen resistance against the pathogen confer pathogen resistance against the pathogen confer pathogen confer plants can be produced by incorporating the gene into plant cells and regenerating plants from the cells; confered the gene into plant ells and regenerating can also be subsequently consequently produced offspring can also be subsequently confered to the gene of the gene in plant cells can confer pathogen configuration of the gene of fragments configuration to the gene or fragments configuration of the gene of fragments confered to reduce gene expression. The nucleic acids/polynucleotides are useful as hybridisation probes to configurate to the gene of plants cells can confered to the gene of fragments conferring pathogen resistance on plants cell fragments conferring pathogen resistance on plants cells and resistance on plants cells and cells and cells and cells and cells and cells can confered to the gene of the cells can confered to the cells can cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confered to the cells can confere
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Best Local Similarity 53.2%;
Matches 133; Conservative
Query Match
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20-NOV-1997.
08-MAY-1997; G01249.
24-SEP-1996; GB-019924.
09-MAY-1996; GB-019924.
(INNE-) INNES CENT INNOVATIONS LTD JC
DIXON MS, HATZIXANTHIS K, JONES DA, WPI; 98-008895/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF-5 pathogen resistance gene variant #2.
Tomato; CF-5 pathogen resistance gene; Cladosporium fulvum-5; tomato leaf mould; Phytophthora resistance; ss.
Lycopersicon pimpinellifolium.
Key
Location/On-1177
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                      7.0%;
53.2%;
  ; Score 62.8; DE; Pred. No. 1.2e. 0; Mismatches
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Pred. No. 1.2e-07;
0; Mismatches 117;
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                                     AATGTTTGGGTAATATCAGTGACCTTCACATTTTGTCGATGTCATCTAATAGTTTCAGAG
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Search completed: June 23, 2000, 22:53:35 Job time: 40611 sec



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Minimum DB
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1: /cgn2_6/ptodata/
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(without alignments)
423.787 Million cell updates/sec
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Listing first 45 summaries
    GenCore version
Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/ina/6_COMB.seq:*
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US-08-666-271-1
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938-534-27
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 Sequence
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/373,375
FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/567,375
FILING DATE: 04-DEC-1995
PRIOR APPLICATION UNBER: US 08/567,375
FILING DATE: 04-DEC-1995
ANTIORNEY/AGENT INFORMATION:
NAME: BASTIAN, Kevin L.
REGISTRATION UNBER: 34,774
REFERENCE/DOCKET NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 32,774
FILECOMMUNICATION INFORMATION:
TELECPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LEMCTH: 1554 base pairs
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US-08-587-680A-24
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Patent No. 5182210	Sequence 3, Appli	Sequence 3, Appli	Sequence 2, Appli	Patent No. 5340934	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 26, Appl	Sequence 47, Appl	Sequence 3, Appli	Sequence 44, Appl	Sequence 41, Appl	Sequence 38, Appl	Sequence 35, Appl	Sequence 1, Appli	-	Sequence 5, Appli

ALIGNMENTS

Sequence 24, Application US/08587680A Patent No. 5977434 GENERAL INFORMATION: ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
STREET: Two Embarcadero SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/587,680A FILING DATE: 17-JAN-1996 TITLE OF INVENTION: Procedures and Materials for TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 27 APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique STREET: Two Embarcac CITY: San Francisco STATE: California USA Ronald, Pamela C. l Townsend Center, E d and Crew LLP Eighth Floor Conferring

023070-058940US

single

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; TYPE: nucleic acid
; STRANDEDNESS: singl
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA (
US-08-587-680A-24
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                                                                                                            CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ronald APPLICANT: Wang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-567-375-3
                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,375
FILING DATE: 04-DEC-1995
                                                                                                                                                                                                                                                                                                                                     ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Procedures and Materials for TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 16
                                             APPLICATION NUMBER: US 08/373,375 FILING DATE: 17-JAN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                             PRIOR APPLICATION DATA:
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              NAME: Bastian, Kevin REGISTRATION NUMBER:
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REFERENCE/DOCKET NUMBER:
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Song, Wen-Yuang
Szabo, Veronique
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          34,774
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023070-058930
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Pred. No. 4.3e-09;
0; Mismatches 115
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Best Local Similarity
Matches 135; Conserv
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APPLICANT:
APPLICANT:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
WOLFORTY
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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                                CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                        CURRENT APPLICATION DATA:
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LENGTH: 3921 base pair
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                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 27
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                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
APPLICATION NUMBER: US 08/373,375 FILING DATE: 17-JAN-1995
                                                                          FILING DATE:
                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                               COUNTRY:
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o. 5977434
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Song, Wen-Yuang
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                                                                        17-JAN-1996
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Pred. No. 1.1e-08;
0; Mismatches 123;
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US-08-475-891A-3
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: LOCATION: join(1..2676, 3520..3918)
: OTHER INFORMATION: /product= "xa-21"
US-08-587-680A-3
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REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
TELEPHONE SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3921 base pairs
                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Ronald,
APPLICANT: Wang, G
APPLICANT: Song, W
                                                                                                                                                                                                                                                 Sequence 3, Application US/08475891A Patent No. 5859339
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Best Local Similarity
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                                               APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/567,375
TITMG DATE: 04-DEC-1995
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
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APPLICATION NUMBER:
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STREET: ...
TMY: San F
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TYPE: nucleic acid
STRANDEDNESS: single
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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Pred. No. 1.1e-08;
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                                                                      Sequence 1, Application US/08475891A Patent NO. 5859339
GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
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Best Local Similarity
Matches 135; Conserv
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NAME/KEY: CDS

LOCATION: jcin(512..3149, 3993..4393)

OTHER INFORMATION: /product= "RRK-B"

OTHER INFORMATION: /note= "xa21 xanthomonas spp. disease

OTHER INFORMATION: resistance gene RRK-B from rice (Oryza

OTHER INFORMATION: sativa)"
        TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 15
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REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1649 TTTCTTGCACTTGAATTGAATAAGATCACAGGAAGCATTCCGAAGGATATTGGCAATCTT 1708
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LENGTH: 5992 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                               493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 tatagtgaactctacaaaaacgagattcaaggaactataccttctgagctttggaaatctg 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                               553 ttgtgtggaacaattcca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 5992 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                         attoctagagaactcacagttatttcaagccttaaagttgttgatgtctcagggaatgat 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ttgggaaaattgaagtcacttgtttttttgcggcttaacgaaaaccgattgaccggtcct 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTGGCTTACAACATCTCTATCTCTGCAACAACAATTTCAGAGGGTCTCTTCCATCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGGGCAGGCTTAAAAACTTAGGCATTCTACTCGCCTACGAAAACAACTTGAGCGGTTCG
                                                                                                                                                                                                                                                                                       TTCAGTGGTTGGATACCA 1906
                                                                                                                                                                                                                                                                                                                                                                   ATCCCGTTGGCCATAGGAAATCTTACTGAACTTAATATCTTACTGCTCGGCACCAACAAA 1888
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Pred. No. 1.4e-08;
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ADDRESSEE:

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. LOCATION: join(1648..4383, 5178..5513)
; OTHER INFORMATION: /product= "RRR-F";
; OTHER INFORMATION: /note= "Xa21 Xanthomonas spp. disease;
; OTHER INFORMATION: resistance gene RRK-F from rice (Oryza OTHER INFORMATION: sativa)"
US-08-475-891A-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
TYPE: nucleic acid
               Sequence 1, Application US/08567375 Patent No. 5952485 GENERAL INFORMATION:
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REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0237
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
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FILING DATE: 06-7UN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
APPLICANT:
                                                                                                                                                                        3046 TTCAGTGGTTGGATACCA 3063
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                                                                                                                                                                                                                                                                                               493 attcctagagaactcacagttattcaagccttaaagttgttgatgtctcagggaatgat 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 aagagtctaatcagtttggatctgtacaacaatctcaccgggaaaatccccatcttct 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
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nes 134; Conserv
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                      ttgggaaaattgaagtcacttgtttttttgcggcttaacgaaaaccgattgaccggtcct 492
                                                                                                                                                                                                                                                           ATCCCATTGGCCATAGGAAATCTTACTGAACTTAATATCTTACTGCTCGGCACCAACAAA 3045
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Pamela C.
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Pred. No. 4.2e-08;
0; Mismatches 124;
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Best Local Similarity
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APPLICATION DATA: 29-SEP-1995
PRIOR APPLICATION DATA: US 08/475,891
APPLICATION NUMBER: US 08/475,891
FILLING DATE: 07-JUN-1995
PRIOR APPLICATION DATA: US 08/373,375
FILLING DATE: 17-JAN-1995
ATPLICATION NUMBER: US 08/373,375
ATPLICATION HOPOMATION:
NAME: Bastian, Keytin L.
REGISTRATION NUMBER: 34,774
REGISTRATION INCREASE 1023070-0588
TELECOMMUNICATION INCREMATION:
TELECOMMUNICATION INCREMATION:
TELECAX: (415) 576-0300
TELECAX: (415) 576-0300
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CURRENT APPLICATION DATA:
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                                                                  2926 TTGGGCAGGCTTAGAAACTTAGGCATTCTAGTCGCCTACGAAAACAACTTGAGCGGTTCG 2985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
493 attectagagaacteacagttattteaageettaaagttgttgatgteteagggaatgat 552
                                                                                                                                                                                                                                                                               313 tatagtgaactctacaaaaacgagattcaaggaactataccttctgagcttggaaatctg 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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LOCATION: join
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Song, Wen-Yuang
                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(1648..4383, 5178..5513)
RMARION: /product= "RRK-F"
RMATION: /note= "Ra21 Kanthomonas spp. disease
RMARION: resistance gene RRK-F from rice
RMARION: (Oryza sativa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-DEC-1995
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                                                                                                                                                                                                                                                                                                                                Score 59.6; DB 4;
Pred. No. 4.2e-08;
0; Mismatches 124;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                           TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
PRIOR APPLICATION UNBER: US 08/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 17-JAN-
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                  LOCATION: join(1648 OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US OF
                                                                                                                                                                                                                                                                                                                                                                            NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 17-JAN-1996
                                                                                                                                                                                                                   TOPOLOGY: 111
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                                                                                  OTHER INFORMATION:
                                                                                                                                                                 NAME/KEY:
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Two Embarcadero Center, Eighth Floor
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Song, Wen-Yuang
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                                                                                                                                                                 CDS
                                                                                                                                 join(1648..4383, 5178..5513)
WATION: /product= "RRK-F"
                                                                                                                                                                                                                  linear
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6.7%;
51.9%;
                                                                               /note= "xa21 Xanthomonas spp. di
resistance gene RRK-F from rice
sativa)"
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Score 59.6; DB 4;
Pred. No. 4.2e-08;
                 Length 6256
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US-08-567-375-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                       TELEFAX: (415) 576-03 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compared operating SYSTEM: PC-DO SOFTWARE: PATENTIA Relicurement Application DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                             REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/567,375
FILING DATE: 04-DEC-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Song, Wen-Yuang APPLICANT: Szabo, Veronique
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                                                                                                                                                                                                                                                      FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 6
FILING DATE: 29-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
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                                      TYPE: nucleic acid
                                                                                                                                                                                                                                NAME: Bastian, Kevin
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                    STRANDEDNESS:
TOPOLOGY:
                                                          LENGTH: 831 base pairs
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Song, Wen-Yuang
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                 single
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                                  PILING DATE: 24-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9409363.0
FILING DATE: 11-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 620-7
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,271
FILING DATE: 19-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HAMMOND-KOSACK, KIM E
APPLICANT: THOWAS, COLWYN M
APPLICANT: JONES, DAVID A
TITLE OF INVENTION: PLANT PATHOGEN RESISTANCE GENES AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/V
FILING DATE: 23-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9:
APPLICATION NUMBER: GB 9:
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  TELEPHONE: 703-816-4091
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nes 129; Conserv
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                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: ARLINGTON STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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n-KOSACK, KIM
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                                                                                                                                                                                              GB 9326428.1
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Pred. No. 2.8e-08;
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Best Local Similarity
Matches 136; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
DATE OF THE PROPER MEDICAL CONTROL OF THE PARTY NOT WITHER. MEDICAL CONTROL OF THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL THE PARTY NOT WELL
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APPLICATION NUMBER: PCT/
FILING DATE: 23-DEC-1994
PRIOR APPLICATION DATA:
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ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PLANT PATHOGEN RESISTANCE GENES TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                   PRIOR APPLICATION DATA:
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                                                                                                 APPLICATION NUMBER: FILING DATE: 24-DEC
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/666,271 FILING DATE: 19-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: ARLINGTON
APPLICATION NUMBER: GB 9409363.0 FILING DATE: 11-MAY-1994
                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tcctagagaactcacagttatttcaagccttaaagttgttgatgtctcagggaatgattt 554
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THOMAS, COLWYN M
JONES, DAVID A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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24-DEC-1993
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; Pred. No. 1.5e
0; Mismatches
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1.5e-06;
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NAME: SADOFF, B.J. REGISTRATION NUMBER:

36,663

620-7

REFERENCE/DOCKET NUMBER:

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; FEATURE:
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; LOCATION:
US-08-666-271-1
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3905 base pairs
                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM; PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                     APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2913 TATCAATCTCTCAAAGAACAGATTTGAAGGTCATATTCCAAGCATTATTGGAGATCTTGT 2972
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                                                                                                                                                                                                                                                                                                                      APPLICANT: Meyerowitz, Elliot M.
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                                                                                          CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3905 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                       ADDRESSEE:
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898..966
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967..3486
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898..3489
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PatentIn Release #1.0,
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Pred. No. 1.8e-06;
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Version #1.30
                                                                                                                                                                     Albritton & Herbert
Suite 3400
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RESULT 12
US-08-238-163-3
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Best Local Similarity
Matches 125; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: BENNET
APPLICANT: LABAVI
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5733 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3360 AATCCC 3365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3120 CTACTACAACAGCTACACCGGTGGTGTTCCACGCGAGTTCGGTGGTTTAACAAAGCTTGA 3179
                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3240 GAAACATCTACATACTCTGTTTCTTCACATCAACAACTTAACCGGTCATATACCACCGGA 3299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     504 actcacagttatttcaagccttaaagttgttgatgttctcagggaatgatttgtgtggaac 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384 cagtttggatctgtacaacaaccaatctcaccgggaaaaatcccatcttttgggaaaaatt 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                564 aattcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 ctacaaaaacgagattcaaggaactataccttctgagcttggaaatctgaagagtctaat 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
                                                                                                    CITY: San Francisco
STATE: California
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TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                    COUNTRY:
                                                                                                                                                                                STREET:
                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATCCTCGACATGGCGAGCTGTACACTCACCGGAGAGATTCCGACGAGTTTAAGTAACCT 3239
                                94105-1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08238163
                                                                                                                                                                            E: Townsend and Townsend Khourie and Crew Steuart Street Tower, One Market Plaza
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2434..5037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BENNETT, Alan
LABAVITCH, John M.
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5117..5467
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Pred. No. 5.5e-06;
0; Mismatches 121;
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SOFTWARE: PAtentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/ACTYMT ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 48.
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                          08-244-646-14
                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                     TITLE OF INVENTION: Nucleotide Sequences Coding An TITLE OF INVENTION: Endopolygalacturonase Inhibitor NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 ggaactataccttctgagcttggaaatctgaagagtctaatcagtttggatctgtacaac 402
                                                                                                                                                                                                                                                                                                                                                                                                                                             913 TTGCTAGCGATGTACTTAGATCGTAACAAACTCACCGGAACAATACCGGAA 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 523 cttaaagttgttgatgtctcagggaatgatttgtgtggaacaattccagta 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463 cggcttaacgaaaaccgattgaccggtcctattcctagagaactcacagttatttcaagc 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
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TOPOLOGY: 11r
                                                   COUNTRY: UZIP: 80303
                                                                                        STATE:
                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGTTGAATTACAATTTACCGGAACAATCCCTTCTTCCCTCTCTCAGCTTCCGAAT 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTAACCTTACAGGTCCGATCCCTGAATTCCTTAGTCAGCTGAAGAATTTGACGTTGCTC 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAACAATTCCACCTGCAATTGCGAAGCTCACAAATCTCAAAATGTTAAGGCTCAGCTTC 792
                                                                                                     Boulder
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                                                                                                                                                                                                                                                                                                                                                           Application US/08244646
                                                                                                                     E: Sally A. Sullivan
5370 Manhattan Circle Suite 201
                                                                     S
                                                                                                                                                                                                                                      Albersheim, Peter
Darvill, Alan
                                                                                                                                                                                                                      Bergmann,
                                                                                                                                                                                                                                                                          Salvi,
                                                                                                                                                                                                                                                                                          De Lorenzo, Giulia
                                                                                                                                                                                                                                                                                                           Cervone, Felice
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421..1401
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Pred. No. 0.01;
0; Mismatches 119;
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APPLICANT: APPLICANT

VASANTHA

NAGARAJAN

APPLICANT

DONALD E. TRIMBUR GREGORY M. WHITED

APPLICANT: APPLICANT:

RICHARD D. LA REAU SHARON L. HAYNIE

MARIA DIAZ-TORRES

APPLICANT:

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RESULT 14
US-08-968-563-5
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LOCATION:
US-08-244-646-14
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Best Local Similarity 50.0
Conservative
                                                        Sequence 5 Patent No.
                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,646
FILING DATE: 06-JUN-1994
               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 06-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/IT/00158
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: SULLIVEN, Sally A.
REGISTRATION NUMBER: 32,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                              319 gaactctacaaaaacgagattcaaggaactataccttctgagcttggaaatctgaagagt 378
                                                                                                                                              439 aaattgaagtcacttgtttttttgcggcttaacggaaaaccgattgaccggtcctattcct 498
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                                                                                                                                                                                                                        379 ctaatcagtttggatctgtacaacaacaatctcaccgggaaaatcccatcttctttggga 438
                                                                                                                                                                                                                                                              835 GATCTGAGGAACAACCGTATCTATGGAACGCTACCTCAGGGACTAACGCAGCTAAAGTTT 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                       Application US/08968563
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(303)499-8089
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1027..1116
CHARLES E. NAKAMURA
ANTHONY A. GATENBY
AMY (KUANG-HUA) HSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phaseolus vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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             NAKAMURA
GATENBY
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Pred. No. 0.18;
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                                                                                                                                                                                                                                                                                                                                                DB 2;
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RESULT 15
5231168-1/c
; PATENT NO. 5231168
; PATENT NO. 5231168
; PATENT NO. 5231168
; PATENT NO. 5231168
; TITLE OF INVENTION: MALARIA ANTIGEN
NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/409,658
; FILING DATE: 18-SEP-1989
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PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 60/030,601
PILING DATE: NOVEMBER 13, 1996
ATTORNEY/AGENT INFORMATION:

NAME: FLOVID, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9982
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEPHONE: 302-892-8112
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1380 Dase Pairs
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Best Local S
Matches 62
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STREET: 1870 SOUTH WINTON ROAD
CITY: ROCHESTER
STATE: NEW YORK
COUNTRY: U.S.
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ORIGINAL SOURCE:
ORGANISM: GPD1
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 INCH DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,563
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CORRESPONDENCE ADDRESS:
CADDRESSE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
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APPLICANT: STEPHEN K. PICATAGGIO
APPLICANT: RAMESCH V. NAIR
TITLE OF INVENTION: METHOD FOR THE RECOMBINANT
TITLE OF INVENTION: PRODUCTION OF 1,3-PROPANEDIOL
                                                                                                                                                                                                                                                                                                  539 GAGCTATCTCCTGTCTAAAGGGTTTTGAAGTTGGTGCTAAAGGTGT 584
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nes 62; Conservative
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Pred. No. 0.25;
0; Mismatches 44;
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nilarity 53.2%;
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Search completed: June 23, 2000, 22:46:00 Job time: 40306 sec

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Title:
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Minimum Maximum

B 80

Total number Searched:

Database :

REFERENCE 1 (bases 1 to 450) AUTHORS Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C. TITLE Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones JOURNAL Plant Physiol. 106, 1241-1255 (1994)	Z	RESULT 1 T04109 T04109 T04109 T04109 T04109 T04109 T04109 T04109 T04109 ACCESSION T04109 T04109 T04109	147.8 16.5 368 64 AW032898 147.8 16.5 423 59 AI774881 147.8 16.5 423 62 AI896737 147.8 16.5 488 64 AW031917 147.8 16.5 497 59 AI772079	155.6 17.4 336 23 H37296 154 17.2 401 37 AA712221 151.6 17.0 612 47 AI496325 149.4 16.7 458 59 AI777982 149.4 16.7 463 74 AW221200 149.2 16.7 463 74 AW221200 149.2 16.7 502 79 AW286582 148.8 16.6 514 35 C22372	171.8 19.2 599 63 AW011134 171 19.1 339 42 AI10079 168.2 18.8 469 63 AI992868 167 18.7 676 74 AW220075 163 18.2 569 59 AI775448 156.6 17.5 423 35 C22371		10 209.6 23.4 5/0 50 AH6/8939 11 208.6 23.3 541 64 AW036865 12 207.8 23.2 637 80 AW350549 13 205 22.9 646 74 AW251939 14 204.2 22.8 545 64 AW037836 15 202.6 22.7 305 25 N65416 16 199.2 22.3 511 74 AW030188 17 197.6 22.1 714 64 AW030188	256.4 28.7 353 23 H37300 223.8 25.0 534 33 AA394359 220.6 24.7 608 81 AW443205 219.6 24.6 720 64 AW031110 213.8 23.9 430 79 AW307218 210.4 23.5 657 80 AW350720	Match Length DB ID 47.0 450 20 T04109 43.3 443 63 AI999615 29.6 556 23 R89998
RESULT 2 AI999615/c AI999615 443 bp mRNA EST 08-SEP-1999 LOCUS 701556713 A. thaliana, Columbia Col-0, rosette-3 Arabidopsis thaliana cDNA clone 701556713, mRNA sequence. ACCESSION AI999615	Qy 384 cagtttggatctgtacaacaatctcacc-gggaaaatcccatcttttt-gggaaaa 441	Qy 264 gaaaacatttacattatcagtcaccatataacattttgctttgagtcatatagtgaact 323		Db 1 GCACGCTCTTCACGCGCTTCGCCGGAGCTTATCAGATCCAGACAATGTTGTTCAGAGTTG 60 Qy 84 ggatccaactcttgttaatccttgttacttggtttcatgtcacttgtaatcaacaccatca 143	Query Match 47.0%; Score 419.8; DB 20; Length 450; Best Local Similarity 98.4%; Pred. No. 3.6e-92; Matches 443; Conservative 0; Mismatches 5; Indels 2; Gaps Qy 24 ggacgctcttcacgcgcttcgccggagcttatcagatccagacaatgttgttcagagttg 83	day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour 119ht cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The library was made in Novagen's Lambda siliques. The library was made in Novagen's Lambda shlox-1 with (oligo dr primed) directional inserts clor between the ECORI and HindIII sites. The library was made in Novagen's Lambda shlox-1 with (oligo dr primed) directional inserts clor between the ECORI and HindIII sites. ORIGIN	/otyginson- restriction /strain-"var columbia" /strain-"var columbia" /db_xref="taxon:3702" /clone-"SCH971P" /clone-Ibb-"Lambda-PRL1" /clone-Lib-"Lambda-PRL1" /note-""vector: Lambda-PRL1 is a cDNA library derived from ec HindIII; Lambda-PRL1 is a cDNA library derived from ec quantitities of 4 pools of mRNA. The mRNA sources were	Tansing,Mi Tel: 517-353-0854 Fax: 517-353-9168 Email: 22313tcn@lbm.cl.msu.edu. FEATURES Location/Qualifiers Source 1450 Location-Tanabidances	MEDLINE 95148729. COMMENT Contact: Thomas Newman MSU-DDE Plant Research Laboratory Michigan State University MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.

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a Shlox-1; Site_1: ECORI; Site_2:
is a CDNA library derived from equal
s of mRNA. The mRNA sources were 1) 7
ated seedlings; 2) tissue culture
ed plants half with 24 hour light
light, 8 hour dark-rosettes; 4)
aerial tissue (stems, flowers and
try was made in Novagen's Lambda
dr primed) directional inserts cloned
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.8; DB 20; Length 450; 3.6e-92; ches 5; Indels 2;
                                             Datcactcttttgccttttgattatct 263
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                                                                                                                                                                                                                                                                                                      tttcaagccttaaagttgttgatgtctcagggaatgatttgtgtgggaacaattccagtag 574
                   ctataaagaagaatgttaggtgaccttgtaagaactctgtaccaagtgttttgtaaatcta 754
                                                                                                                  | cagaactactaggtcttgcgagctatgacaccaattgcacttaaaaagaagttgaagaac
                                                                                                                                                                                      AAGGACNTTTTGNANACATTCCTATGCNNAACTTTGAGNACAACCTGAGATTGGAGGGAC
                                                                                                                                                                                                               TTTCAAGCCNTAAANTNGTTGATGTCTCAGNGAATGATNTGTGTGGNACAATTCCAGTAG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388;
                                                                                            CAGAACTACTAGGTCTTGCGAGNTNTGACACCAATTGCACTTNAAAAGAAGTTGAAGAAC
                                                                                                                                                                                                                                                                                                                                                                         TTTTTTGCGGCTNAACGAAAACNGATNGACNGGTNNTATTCCTAGAGNACTCACAGTTA 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana Gene Expression MicroArray Unpublished (1999)
On Mar 10, 1998 this sequence version replaced of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte
Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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314-427-3324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Vector: psport; Site_1: NotI; Site_2: SalI; CDNA library was derived from untreated rosette tissue from Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks. Plants were grown in 1:1:1 peat moss/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C under constant light, and watered with fertilizer. CDNA synthesis was initiated using a NotI-oligo(dT) primer. Double-stranded cDNA was blunted, ligated to SalI adaptors, digested with NotI, size-selected, and cloned into the NotI and SalI sites of the psport vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="A. thaliana, Columbia Col-0, rosette-3"
/tissue_type="rosette"
/dev_stage="4 - 7 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cultivar="Columbia Col-0"
/db_xref="taxon:3702"
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90.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 387.4; DB 63;
Pred. No. 2.8e-84;
0; Mismatches 42;
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REFERENCE
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313 tatagtgaactctacaaaaacgaagattcaaggaactataccttctgagctttggaaatctg 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
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                                                     Local Si
hes 335;
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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16353 Lambda-PRL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Apr 14, 1993 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McIntosh,L., Ohlrogge,J.,
Retzel,E. and Somerville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R89998.1
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                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 517-353-0854
: 517-353-9168
il: 22313tcn@ibm.cl.msu.edu
primer: T7 dye_primer.
                                                                                                                                                                 151
                                                   29.6%;
larity 80.0%;
Conservative
                                                                                                                                                         /clone_lib="Lambda-PRL2"
//clone_lib="Lambda PRL2"
//note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_2: Not;
/note="Vector: lambda Zip-Lox; The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA."

51 a 118 c 123 g 146 t 18 others
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis t
/strain="var columbia"
/db_xref="taxon:3702"
/cione="187H5T7"
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Arabidopsis thaliana
                                                   Score 265; DE
Pred. No. 1.6e
0; Mismatches
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Raikhel, N.,
                                                   DB 23;
..6e-54;
nes 79;
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., Somerville,S., Thomashow,M.,
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187H5T7, mRh
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49

TATCTAGAGCTCTACAAAAACAACATCCAAGGAACTATACCTTCCGAACTTGGAAATCTG 108

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VERSION
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H37300
H37300.1
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On May 8, 1995 this sequence version replaced g1:801146.
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PL, Michigan State University, Plant Biology Bldg., E.
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15429 Lambda-PRL2
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Arabidopsis thaliana
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McIntosh, L., Ohlrogge, J., R:
Retzel, E. and Somerville, C.
                                                                                                                                                                                                                                                                                                                                                            Seq
                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 517-353-0854 Fax: 517-353-9168
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/clone_lib="Lambda-PRL2"
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                                                                                                                                                                     Lansing, Mi
Tel: 517-35
                                                                                                                                                                                                                                                                                                    Newman,T., deBruijn,F.J., Green,P., Reegstra,K., Kende,H. McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thom Retzel,E. and Somerville,C. Genes galore: a summary of methods for accessing results large-scale partial sequencing of anonymous Arabidopsis c plant Physiol. 106, 1241-1255 (1994)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
euphyllophytes; Spermatophyta; Magnollophyta; Brassicaceae;
                                                                                                                                                                                                                                                 On May 18, 1995 this sequence version
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
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a 85 c 67 g 89 t 14 others
/organism="Arabidopsis t
/strain="var columbia"
/db_xref="taxon:3702"
/clone="305G1T7"
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0; Mismatches
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,S., Thomashow,
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                                                                                                    D'Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Hansen,T.S., Ronning,C.M., Craven,M.B., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D., Giovannoni,J.J. and Martin,G.B. Generation of ESTs from tomato callus (mixed elicitor) Unpublished (1999)

On Dec 20, 1995 this sequence version replaced gi:1135853. Contact: David Frisch
                                                                                                                                                                                                                                                                                               Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                       Clemson University
100 Jordan Hall, C
                                                                                           Clemson University Genomics Institute
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               864 656 4366
864 656 4293
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/note="Yector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Yector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA. "
51 a 114 c 125 g 126 t 18 others
dfrisch@CLEMSON.EDU
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Pred. No. 1.7e-44;
0; Mismatches 65
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/tlssue_type="leaf"
/dev_stage="4-5 week old plants"
/lab_host="XL1-Blue MRF"
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/db_xref="taxon:4081"
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Pred. No. 1e-43;
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 <u>agtgaactctacaaaaacgagattcaaggaactataccttctgagcttggaaatctgaag</u>
                                                            gattatctgaaaacatttacattatcagtcacacatataacattttgctttgagtcatat
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Clemson University
100 Jordan Hall, Clemson, SC 29634, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generation of ESTs from tomato callus tissue Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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864 656 4293
l: dfr1sch@CLEMSON.EDU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="tomato callus, TAMU"
/tlssue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XL1-Blue MRF/"
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/cultivar-"TA496"
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                                                                                                                                                                                                                                                                                                                                                    Score 219.6; DB 64;
Pred. No. 1.8e-43;
0; Mismatches 129;
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On Dec 20, 1995 this sequence version replaced gi:113369(
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
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Glycine max
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This clone is available through: Genome Systems, Inc.
This clone is available through: Genome Systems, Inc.
Parkway Circle St. Louis, Missouri 63134 For further i
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3
427-3334 or contact: clones@genomesystems.com or
infogenomesystems.com web site: www.genomesystems.com
seq primer: -40RP from Gibco
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Fax: 314 286 1810
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/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
XhoI; The mRNA was isolated from entire roots of
2-month-old 'Williams' plants that were greenhouse grown
                                                                                                                   /clone="GENOME SYSTEMS
/clone_lib="Gm-c1009"
                                                                                                                                                                                   /organism="Glycine max"
/db_xref="taxon:3847"
                                                                                         /lab_host-"XL10-Gold"
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soybean
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in 5-gallon pots. To suppress nodulation, Black Gold Al-Purpose potting soil was supplemented with: 0.36g/L available phosphoric acid (P205), 20mg/L urea N, 0.16g/L S, 0.49mg/L B, 2.5mg/L Cu, 0.15g/L Fe, 13.53mg/L Mn, 0.26mg/L Mo, 14mg/L Zn, 20mg/L Ca, and the following
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Pred. No. 4.5e-42;
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                                                                                                                                                                                                                           aagagtctaatcagtttggatctgtacaacaaccattctcaccgggaaaatcccatcttct
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                                                                                                                                                                     AAGAGTCTAGTTAGCTTGGACTTGTACAACAACAACATATCAGGCACCATCCCACCTTCA 415
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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134. For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888)919-3324 or (314)
427-3324 or contact:clones@genomesystems.com or info@genome
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Edwin R. Madigan Building,
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Seq primer: 5'-TTTTTTTTTTTTTTTTTT(A/C/G)-3'.
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Center for Comparative and Functional
University of Illinois,
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131 c 120 g 191 t 25 others
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Tel: 650 723 2227
Fax: 650 725 8221
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Contact: Walbot
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/db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone_lib="605 - Endosperm cDNA library from Schmidt tax/
/clsue_type="nucellar, embryo, and endosperm"
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/dev_stage="10-14 days post-pollination"
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/note="Organ: Kernel; Vector: pAD-GAL4-2'; Site_1: EcoRI;
/note="Organ: Kernel; Dector: pad-GAL4-2'; Site_1: CoRI;
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Stanford University
855 California Ave, Palo Alto, CA 9
Tel: 650 723 227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 614019 row: G column: 10.
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Contact: Walbot V
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/note="form="
                                                                                                                                                                                                                                               Lab
                                                                                                                                                                                                                                                           /note="Organ: root; Vector: pBlueScriptII SK+;
EcoRI; Site_2: XhoI; 3-4 days old root tissue:
                                                                                                                                                                                                                                                                                                                                                             /organism="Zea mays"
/cultivar="W23"
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/clone_lib="614 - roo"
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Erpelding, J., Raph, C., Shoop, E., Pardinas, J., Liu, L. and I
A Functional Genomics Program for Soybean (NSF 9872565)
Unpublished (1999)
On May 18, 1998 this sequence version replaced gi:3136929,
Other ESTS: A1495378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae;
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Tel: (217) 244-6147
Fax: (217) 333-4582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Vodkin, L.O., PI, A Functional Genomics Soybean (NSF 9872565)
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/clone_lib="Gm-r1021"
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                                                                                                                                         Giovannoni,J.

Generation of ESTs from tomato fruit tissue
Unpublished (1999)
                                                                                                                                                                                                             Lycopersicon.

1 (bases 1 to 646)

Alcala, J., Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F. Alcala, J., Vrebalov, J., White, Rowman, C.L., Ahn, S., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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EST298750 tomato fruit red ripe,
                                          Clemson University
100 Jordan Hall, C
                                                                                                                      On Jul 8, 1999 this s
Contact: David Frisch
                                                                                         Clemson University Genomics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.life.uiuc.edu/biotech/keck.html."
112 c 127 g 188 t 25 others
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                                            Clemson,
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Pred. No. 1.3e-40;
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                                                                                                                                                      cctagagaactcacagttatttcaagccttaaagttgttgatgtctcaggggaatgatttg
                                                                                                                                                                                                                                                                                                                     agtgaactctacaaaaacgagattcaaggaactataccttctgagcttggaaatctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                 GAGCTCGGAAAGCTTGAACATCTACAGTATCTG------
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                                                                                  TGTGGAACAATTCCTACTTCTGGTCCATTTGAGCATATT 646
                                                                                                          tgtggaacaattccagtagaaggaccttttgaacacatt 594
                                                                                                                                       CCAAGAGAACTTACTAGCATTTCTAGCCTGAAAGTTGTGGATGTCTCGAATAATGATTTG
                                                                                                                                                                                             GGAAACCTGAAAAACCTTGTTTTCTTGCGTCTAAATGATAACAAGCTAACAGGACCAATC
                                                                                                                                                                                                             ggaaaattgaagtcacttgtttttttgcggcttaacgaaaaccgattgaccggtcctatt 495
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/db_xref="tax201"
/clone="cleN6M3"
/clone="cleN6M3"
/clone="lib="tomato fruit red ripe, TAMU"
/tissue_type="pericarp"
/dev_stage="red ripe (7-20 days post-breaker)"
/dev_stage="red ripe (7-20 days post-breaker)"
/dev_stage="red ripe (7-20 days post-breaker)"
/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Giovannoni; Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
81 a 126 c 138 g 201 t
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/cultivar-"TA496"
  tomato mixed
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Pred. No. 6.3e-40;
0; Mismatches 115;
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313 tatagtgaactctacaaaaacgagattcaaggaactataccttcttgagcttggaaatctg
                                                    613 aacaacctgagattggagggaccagaactactaggtcttgggagctatgacaccaattgc 672
68 TATCIGGAGCITTACAAAAATAATATICAGGGAACCATCCCTAAAGAGCICGGTAACTIG 127
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                                                                                                                                                                                                                              ttgtgtggaacaattccagtagaaggaccttttgaaccacattcctatgcaaaactttgag
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Clemson University
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On Jun 22, 1998
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Generation of ESTs from tomato leaf tissue
Unpublished (1999)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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AW037836.1 GI:5896590
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/fissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XL1-Blue MRF'"
/lab_host="XL1-Blue MRF'"
/lab_host="XL1-Blue MRF'"
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/cultivar="Rio Grande PtoR"
/db_xref="taxon:4081"
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Pred. No. 9.8e-40;
0; Mismatches 118;
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Matches 235;
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502 gaactcacagttatttcaagccttaaagttgttgatgtctcagggaatgatttgtgtggga 561
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MSU-DOE Plant Research Laboratory
Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,
McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,
Retzel,E. and Somerville,C.
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primer: T7 dye primer.
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517-353-9168
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a 68 c 63 g 81 t 12 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis thaliana"
/strain="var columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Lambda-PRL2"
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Pred. No. 2.3e-39;
0; Mismatches 65;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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De, V.S., Schmidt, E.D., Van, H.G. al PRODUCTION OF APOMICTIC SEED PATENT: WO 9743427-A 20-NOV-1997;
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De, V.S., Schmidt, E.D., Van, H.G. a
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CIBA GEIGY AG (CH)
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De, V.S., Schmidt, E.D., Van, H.G. a
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gctttgattcacctggtcgaagcaaactccgaaggagatgctctttacgctcttcgccgg
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De, V.S., Schmidt, E.D., Van, H.G. and PRODUCTION OF APOMICTIC SEED Patent: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
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LYKNNIGGTIPSELGNLKNLISLDLYNNNLTGIVPTSLGKLKSLVFLRLNDNRLTGPI
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De, V.S., Schnidt, E.D., Van, H.G. a
PRODUCTION OF APOMICTIC SEED
Patent: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
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/protein_id="CB42250.1"
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ESYSELYKNEIQGTIPSEIGNLKSLISLDLYNNNLTGKLPSSLGKLKSLVFLRLNENR
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                                                                                                                                                                                                           caaggaactataccttccgaacttggaatatctgaagaatctcatcagcttggatctgtac
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agccttaaagttgttgatgtctcaagcaatgatttgtgtggaacaatcccaacaaacgga
                                                            gcgcctgagcttgggaagcttgaacatttacagtatctagagctctacaaaaaacaacatc
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Brabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphylicphytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
euphylicphytes; Spermatophyta; Magnoliophyta; Erassicaceae;
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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De, V.S., Schmidt, E.D., Van, H.G. a
PRODUCTION OF APOMICTIC SEED
Patent: WO 9743427-A 20-NOV-1997;
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/translation="messyvvetllslillpnhslwlasanlegdalhtlrvtlydpn

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pedppystlgolkreslelgvasdgfsnknilgrggfglykndsvaksclrerp

psgppldwptkrrilghglyklbhedpriithrygaanilldeefaavgdfgl

aklmdykdthyttavrgtighiapeylstgkssektdvfggimllelitggrafdla

rlandddymlldwykgllkekklemlydpdlotnyebreledyigvallctogspmer
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/db_xref="taxon:3702"
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/db_xref="GI:4756650"
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                     caagacaaccgcgtcactcgtgtggatttggggaattcaaacctctctggacatcttgcg
                                                                     CTGCAGAGCTGGAATTCGACGCTTGCCAATCCCTGCACCTGGTTCCATGTCACCTGCAAC
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                                                                                                                                               AACACTGAAGGTGACATACTGTACAAGCAAAGGTTGGCATGGGAGGACCCAAACAACGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (26-JUN-1996) John D. Hipskind, Botany and Plant Pathology, Purdue University, West Lafayette, IN 47907, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erratum:[[published erratum appears in Mol Plant Microbe Interact
1997 Mar;10(2):302]]
2  (bases 1 to 936)
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otein mRNA, complete c
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/db_xref="GI:1710124"
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ussileskloenslagaipasignikaloeskludnmltgtvpsksfplstegnltel
ntdrileskloenslagaipasignikaloeskludnmltgtvpsksfplstegnltel
ntdrinldgtrtssglrvtaiiodalkta"
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232 c 207 g 250
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/note="leucine-rich repeat-containing extracellular
/lycoprotein; contains six N-glycosylation sites
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12. .755
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/db_xref="taxon:4558"
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Pred. No. 1.2e-29;
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1 (bases 1 to 1755)

Schmidt E.D., Guzzo, F., Toonen, M.A. and de Vries, S.C.

A leucine-rich repeat containing receptor-like kinase marks somatic plant cells competent to form embryos
Development 124 (10), 2049-2062 (1997)

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Schmidt, E.D.L., Guzz
Direct Submission
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Submitted (12-MAR-1997) Molecular Biology, Ag
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PGQNRFTGAIAGGVAAGAALLFAAPAMAFAWWRRRKPREHFFDVPAEDDPEVHLGQLK
RFSLRELQVATDTFSTILGRGGFGKVYKGRLADGSLVAVKRLKEERTPGGELQFQTEV
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/protein_id="AAB61708.1"
/db_xref="GI:2224911"
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KSLLKEKKLEMLVDPDLENNY IDTEVEQLIQVALLCTQGSPMERPKMSEVVRMLEGDG
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/db_xref="taxon:4039"
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Score 103.4; DB 8; Pred. No. 2.4e-16; 0; Mismatches 161;

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.

1 (bases 1 to 1815)
10e.V.S., Schmidt,E.D., Van,H.G. and Hecht,V.F.
PRODUCTION OF APOMICTIC SEED
Patent: W0 9743427-A 20-NOV-1997;
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Pred. No. 2.4e-16;
0; Mismatches 161;
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L.esculentum LRP gene
X95269
X95269.1 GI:1619299
                                                                                                                                                                                                                                                                                    Submitted (18-JAN-1996) P. Vera, Universidad Politecnica de Valencia, Inst. de Biologia Molecular y Celular de Plantas, C de Vera 14, E- 46022 Valencia, SPAIN 2 (bases 1 to 4604) Tornero, P. Mayda, E., Gomez, M.D., Canas, L., Conejero, V. and V Characterization of LRP, a leucine-rich repeat (LRR) protein tomato plants that is processed during pathogenesis Plant J. 10 (2), 315-330 (1996)
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join(113. .34
4283. .4355)
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            /codon_start=1
/product="LRR protein"
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/db_xref="GI:1619300"
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 _xref="SPTREMBL:Q96477"
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AC009991
AC009991.3 GI:6016677
HTG.
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Arabidopsis.

1 (bases I to 101284)

Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H.,

Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Ba

Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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/gene="LRP"
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/gene="LRP"
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/gene="LRP"
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Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RN/RepeatMasker.html). Regions of http://ftp.genome.washington.edu/RN/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur.epm.ornl.gov). Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), and NetPlantGene, http://gnomic.stanford.edu/-chris/GENSCANW.html), and NetPlantGene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROCKWILE, MD 20850, USA
e-mail: xiin@tigr.org
BAC clone F9F8 is from Arabidopsis chromosome III and is near the
molecular marker g4547.
The orientation of the sequence is from SP6 to T7 end of the BAC
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Direct Submission
Submitted (09-SEP-1999) The Institute for Genomic Research,
Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org
3 (bases 1 to 101284)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genomic sequence that are not annotated as genes but
exons by GRAIL are annotated as misc features.
   Location/Qualifiers
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The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana chromosome III BAC F9F8 genomic sequence Unpublished
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                                                                                                             854. 973
/note="exon predicted by xgrail, complement(1182. 1357)
/note="exon predicted by xgrail, marginal_shadowexon"
                     complement(1516...1694)
/note="exon predicted by
excellent_shadowexon"
1546...1666
                                                                                                                                                                                                                                                        /note="ex
672..752
                                                                                                                                                                                                                                                                                                                        /note="exon predicted by
excellent_shadowexon"
                                                                                                                                                                                                                                                                                                                                                                   /note="exon predicted by xgrail, complement(347. .408)
                                                                                                                                                                                                                                                                                                                                                                                                                /note="exon predicted by xgrail, quality excellent"
124. .259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="g4547"
/clone="F9F8"
                                                                                                                                                                                                                              /note-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:3702"
/chromosome="III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis
/note="exon predicted by xgrail, quality good"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cultivar="Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                .108
                                                                                                                                                                                                                              exon predicted by xgrail,
                                                                                                                                                                                                                                                                           exon predicted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thaliana"
                                                                                                                                                                                                                                                                                                                                                xgrail,
                                                                    xgrail, quality
                                                                                                                                                                                                                                                                         xgrail,
                                                                                                                                       quality
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/note="exon
                                                                                                                         complement(<9426. .>11865)
/gene="F9F8.3"
/note="similar to leucoanthocyanidin dioxygenase B:BAA20143 [Perilla frutescens]"
complement(join(9426. .9674,10198. .10528,11098. 11491. .11865))
/gene="F9F8.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene-"F9F6.2"
/note-"similar to nucleic acid binding protein Alfin-1
GB:AAA20093 [Medicago sativa]"
join(5696. .5795,5897. .5929,6013. .6235,7264. .7387,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="exon predicted by xgrail, quality excellent" complement(2090, .2250) /note="exon predicted by xgrail, quality good_shadowexon" 2114. .2246
                                                                                                                                                                                                                                                                                                                                                                                                                 KCVKITPAKAESIKQYKCPPCCAKKGRQ"
complement(7717...7760)
/rpt_family="(CAT)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MYGPARPQIVLFGSSIVQMSFGHGGWGAILSEVYARKADIILRG
YYGWNSSRALEVVDQVFFKDAAVQFSLVIVYFGGNDSMAPHSSGLGPHVPLTEYVDNM
KKIALHLQSLSDFTRIIFLSSPVDEBAVVRQNQSPYLSEVIRTNDLCKTYSDACVELC
QELGLEVVDLFSTFQKADDWKTVCFTDGIHLSAQGSKIVAGEILRVVKEAEWHPSLHW
KSMCTEFADDSPYDLVSADGKQTVNSSEWTYFWEEQWD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(3070. .3325,3565. .34506. .4655,4800. .>5013)
/gene="F9F8.1"
/product="putative leucoanthocyanidin dioxygenase"
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/translation="MNNLDEIKIESKTCLNDQEQEVKIDNMHMSDQDKNKIEIKNKSG
/translation="MNNLDEIKIESKTCLNDQEQEVKIDNMHMSDQDKNKIEIKNKSG
                                                                                                                                                                                                                                                                                                                                                                                                  complement(7810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKENLCLYGHPNESWEVNLPAEEVPPELPEPALGINFARDGMORKDWLSLYAVHSDCW
LLSVSFYFGARLNRNERKRLFSLINDLPTLFDYVTGRKAMKDNKPSSDSGSKSRNGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative nucleic acid binding protein"
/protein_id="AAF01506.1"
/db_xref="GI:6016679"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="exon predicted by xgrail, quality excellent_shadowexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(5527. .5579)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (5513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="exon predicted by xgrail,
                                                                                                                                                                                                                                                                      /gene="F9F8.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSIDGQTKSSTPKLMEESYEEEEEEDEHGDTLCGSCGGHYTNEEFWICCDVCERWYHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="F9F8.2"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAF01505.1"
/db_xref="GI:6016678"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F9F8.1"
/note="unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(3215. .3325,3565. .4506. .4655,4800. .5013)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="F9F8.1"
/note="similar to unknown protein GB:AAC27167 [Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MAAAAVSSNPRTVEEIFKDYSARRAALLRALIKDVDDFYSQCDP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oin(5589.
                                                                                                                                                                                                                                                                                                                                                                          lement(7810. .7847)
_family="(GAAAA)n"
                                                                                                                                                                                                                                                                                                                                                                                             _family="(CAT)n"
lement(7810
                                                                                                                                                                                                                                                                                       _family="(TAA)n"
lement(join(<9426. .9674,10198. .10528,11098. .11345,
1. .>11865))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _family="(GA)n"
ement(scale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family="(CAAA)n"
3070. 2275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F9F8.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .5795,5897. .5929,6013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .3642,4094. .4234,4338. .4414,
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Best Local (
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    complete sequence
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/protein_id="aaf01508:1"
/protein_id="aaf01508:1"
/db_xref="G1:6015681"
/translation="manuvlsecgirplpriyttprsnetsnetsnunkerpslsssykts
ssplsetingloftenmalavstplttplfeespleednkqredpgapppenladir
aaipkhcwyknpwkslsyvvrdyaivfalaacaaylnnwivwplymlaggtmfwalfy
lghdcghgsfsndpklnsvvghllhssilvpyhgwrishrthhqnhghvendeswhpm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(13367. .13468)
/note="exon predicted by xgrail, quality marginal"
complement(13742. .13788)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12824. .12836
/note="exon predicted marginal_shadowexon"
                                                                                                                                                                                                                                                                                                                                                           complement(join(13988. .14179,14261. .14398,14502. .14582, 14676. .14861,14941. .15033,15124. .15190,15272. .15361, 15662. _.16155))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="exon predicted by xgrail, quality marginal" complement(join(13822. .14179,14261. .14398,14502. .14582, 14676. .14861,14941. .15033,15124. .15190,15272. .15361,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKLGGRLMTILSSNLGLRAEQLQEAFGGEDVGACLRVNYYPKCPQPELALGLSPHSDP
GGMTILLPDDQVVGLQVRHGDTWITVNPLRHAFIVNIGDQIQILSNSKYKSVEHRVIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="identical to omega-3 fatty acid desaturase, chloroplast precursor GB:P46310 [Chloroplast Arabidopsis thaliana]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11962. .11996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFSGNEDDKKRISEACREWGFFQVINHGVKPELMDAARETWKSFFNLPVEAKEVYSNS
PRTYEGYGSRLGVEKGAILDWNDYYYLHFLPLALKDFNKWPSLPSNIREMNDEYGKEL
SEKIYNTLDKPTRFFRFTLPLVMLAYPFYLWARSPGKKGSHYHPDSDLFLPKERKDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSEKERVSLAFFYNPKSDIPIQPMQQLVTSTMPPLYPPMTFDQYRLFIRTQGPRGKSH
                                                                                                                                                                                                                              /product="omega-3 fatty acid
precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(13822. .16380)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15662. .16380))
/gene="F9F8.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="F9F8.4"
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                                                                                                                                                                                                                                                                                                                                   'gene="F9F8.4'
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                                                                                                                                                                                                                                                             chloroplast
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44816 TCTTACAGGTTGATTCCAATAAGCTCAGTGGAAATGTTCCCCATCTCACTACTGAATTTGA 44757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44936 TCTTTGGTCAGATTCCATCTTCGATTGGGAACCTTGCTCGTCTCACCTATCTCTACCTTT 44877
                                                                                                                                                                                                                           44696 TCAGTTTACTATCAAACTTGATGGACTTTGAAGCAAGTAACAACGCTTTCACTGGAACTC 44637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44876 CITACAACAATTTCGTTGGTGAAATCCCATCTTCTTTTGGCAATCTAAACCAGCTGATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 acaaaaacaaca;ccaaggaactataccttccgaacttggaaatctgaagaatctcatca 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 tototggacatottgogoctgagottgggaagotttgaacatttacagtatotagagotot 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 8.0%;
Local Similarity 54.9%;
                                                                                                                                        TCCC 44633
                                                                                                                                                                                                                                                          tcactgcaatcccaagccttaaagttgttgatgtctcaagcaatgatttgtgtggaacaa 649
                                                                                                                                                                                                                                                                                                                                              gcttggatctgtacaacaatcttacagggatagttcccacttctttgggaaaattga 529
                                                                                                                                                                                                                                                                                                                    CGAGGTTGTCTGCTTTATTACTTTCCCACAATCAGTTCACAGGCACGATTCCTAATAACA 44697
  AC008017 116944 bp
Arabidopsis thaliana
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  chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 84.8; DB 8; Pred. No. 1.7e-11; 0; Mismatches 137;
  н
  BAC
  PLN
: F3N23
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18-SEP-1999 genomic sequence,
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AC008017.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Chen, S., Harman, P., Hicks, R., Huerta, M., Mason, S., Espel, J., Zimmernan, M., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskala, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (18-SEP-1999) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Brooks, S., Buehler, E., Chao, Q., Dunn, P., Gonzalez, A., Khan, S., Kremenetskala, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shin, P., Toriun, M., Vyotskala, V., Yu, G., Ecker, J., Theologis, A. and Tayla B. W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (15-JUL-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-JUL-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Federspiel, N.A., Palm, C.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 116944)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15,
                                                                                                                                                                                       /note="818 identical to threonine synthase [Arabidopsis thaliana] (g1|4914408). Location of ests GBGF589 3' (gb|F15267) and GBGe175 (gb|Z26034)" /codon_start=1
                                                                                                                                                                                                                                                                                                    complement(join(1333. .2271,2355. .2966))
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism-"Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome-"I"
                                                                                                                                                                                                                                                                                                                                                                                                                /clone-"F3N23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1999 this sequence version ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              replaced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gi:5441915
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S., Harman, P.
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/transiatation="masssssatrlhydyflsfrgvdtrqtivshlyvalrungvl
trkndrkleigdtiadelvkalotskfavilsenvarstrvcleelklikolhsergi
kvlpifygvkrsdvrvqegsfatafgsvbleadmiaevvggissklprmkstdlililvg
meahmxkmilliniggedevhulgingskgigkstiakclydrfsrgfpahcflenvs
kgydikhloksellshliydedvelwsheagsgeikerlghkyvpvldvvvkvedlhg
kakdpskefgrstiittrdkgllnscgvnivfvkclddkdalqvfkklafgrpps
dgfedlfirasrlahglpsalvafashlsaivaldewedellallengkvvvldvrolg
grounitevkclddkdalfolystr
hillvotgreivrgeskriittriperfrhiktroppteihtryldbriklghakclvnisidgcism
hillvotgreivrgeskorferdpteihtryldbriklghakclvnisidgcism
sydgldqydktvflhvacffngghlryiraflkncdarinhlaakclvnisidgcism
hillvotgreivrgeskorferdpteihtryldbriklghakclvnisidgcism
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hillvotgreivrgeskorferdstriklghakclvnisidgcism
syngklamgtrildliggnbrylppsmgolamiktislsncrrikalpglsqverlvlsg
dicqlolletldiggnbrylppsmgolamiktislsncrrikalpglsqverlvlsg
cvkrlgslmgilgagrynildpfcyekcksigslkgilsversapperneilelslelengs
cvkrlgslmgilgagrynildpfcyekcksigslkgilsversapperneilelslelengs
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/gene="F3N23.3"
complement(join(8272. .8658,8746. .8916,
9161. .9252,9364. .9661))
/gene="F3N23.3"
/note="99% identical to Transcription fathaliana] (gil2398525)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="F3N23.2"
6030. 7079
/gene="F3N23.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="F3N23.4"
complement()oin(12076. .12519,12613. .13851,13955. .14140,
14368. .15451,15672. .16057))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MMHQMLNKKDSATHSTLPYLNTSISWGVVPTDSVANRRGSAESL
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MYSMLPGRVPLPAELTETDPYPVNAKOYHAIMERRQQBAKLEAQNKLIKARFPLHES
RHYHALKRPRGSGGRFLNTKKLLQESEQAAAREQEQDKLGQQVNRKTNMSRFEAHMLQ
NNKDRSSTTSGSDITSVSDGADIFGHTEFQFSGFPTPINRAMLVHGQSNDMHGGGDMH
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VLDGEDSSNNGKRGPSIGQTVRNLVREGGWTACYRGLGPRCASMSMSATTMITTYEFL
KRLSAKNHDGFYSKS"
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HLIREVTAELPIYLANSLNSLRLEGGKTAAIEILQQFNWQVPDWVIVPGGNLGNIYAF
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LYPAYLMKTRQQVCHSQGSCIKTAFTLYRHEGIKSTKGFGTSLMGTIPARALIMTAL
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LVNASRCNYVNGFDAFRKIVRADGPKGLYRGFGISILTYAPSNAVWWASYSVAQEMVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(12076. .16057)
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DPVSIDRAVYALKKSNGIVEEATEEELMDATALADSTGMFICPHTGVALTALMKLRKS
HIQVPEPGDEIILCGVEHVGFVLK"
16543. .17907
                                                                                                                 LVSLSEELSHFTKLTYLDLSSLEFRRIPTSIRELSFMRTLYLNNCNKIFSLTDLPESI
KYLYAHGCESLEHVNFSSNHSFNHLDFSHCISLECISDLVRDEMNEEYSQEAPFRLVC
ITKYSIASTNNMRTSWREPMRIKLPKIKAAPKLVGFFVQIMVVCEKPFHLQFPAFSYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="Similar to disease resistance proteins"
/protein_id="AAD55631.1"
/db_xref="GI:5903073"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Similar to disease resistance proteins RPP1-WSB
(g1|3860165), RPP1-WSC (g1|3860167) and RPP1-WSA
(g1|3860163) [Arabidopsis thaliana]."
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/protein_id="AAD55630.1"
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/db_xref="GI:5903071"
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(gb|H77203) and 205D12XP 3' (gb|AA605559)"
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Matches
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                                                                                                                                                                                                                                                                                                                                                     263 caactcttgttaatccttgtacctggttccatgtcacctgtaaccaagacaaccgcgtca 322
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Sinhes 210;
                                                                                                                                                                                                                                                                                                                       CATCTGAAGCCACTCCATGTAACTGGTTTGGTATTATCTGTGATGATTCTAAGAAGGTTA 84582
                                              GTTTAGGGAAACTGTAGCTCACTTGTGTACATTGATTTGTCTGAAAATAGTTTCTCTGGTA
                                                                                         aacttggaaatctgaagaatctcatcagcttggatctgtacaacaacaatcttacaggga 502
                                                                                                                                        TCAAAAGCTTAGAGATATTGGATATGAGTTCTAACAATTTCTCTGGGATTATACCTTCCA 84702
                                                                                                                                                                                                                              CGTCTCTCAACTTCACCGGTTCAGGTGTTTCAGGCCAATTGGGTCCTGAAATAGGGCAAC
                                                                                                                                                                                                                                                         ctcgtgtgggatttggggaattcaaacctctctggacatcttgcgcctgagcttgggaagc 382
tagttcccacttctttgggaaaattgaagtctctggtcttttttacggcttaatgacaacc 562
                                                                                                                                                                   ttgaacatttacagtatctagagctctacaaaaacaaccatccaaggaactataccttccg 442
                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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MIEBIVKDISKKLLIMOPVDFSDIVGMMAHMERLSPLLSMISENEVRNIGJYGMGGIG
KTTIAKCLEDQFSQGFPARCFLENVSKIYRKGGVSSLAEKFLSTTLGLSKKMKGSGV
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GVRTVYEVKCMDNDALACFIENVSLIYRKGHVSSLAEKFLSTTLGLSKKMKGSGV
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GVRTVYEVKCMDNDALACFIENDDESVMEILKISTDGLEETDKNVFLHVACLFNGEPLR
RATTILDDGVLAGGLGLKTIAERSLIETTASGYIKMHUVDQTARAIVNQESWQRHG
RGYUMNPYEIYELLKRNTPODLVBIILHRSNLTSFWKETVYKALNRSMLTPMYLLVLN
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ISYLTRLTTIDVSYCEELASYITIRECHEDLYBGLSMAVNLEELITAMLSKGINH
IQMFWLDGNVGHLSFTTEQQGFDKLTKKEKQQALGFLFEFGQGSYKKA
QGKSQFTSKFHGFTSVDISHFRYSSDGASFLCFSLSKFPCVKEILLIMIKKYIDDV
CGLKFLEKLDWSGNDFEILPETMMQRDDLAFDNQALEFSTRTRQALOFLPEFHGQESVKKA
QGKSQFTSKFHGFTSVDISHFRYSSDGASFLCFSLSKFPCVKEILLIMIKKYIDDV
CGKFTEKLDWSGNDFEILPETMMQRDDLAFDNGALEFLENGLFFLFEFTKLSGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEITSKKYIKWANALIANIA (19050. .23350)

/gene="F3N23.6"
/gene="F3N23.6"
/complement(jotn(19050. .19667,19764. .21344,21686.
22887. .23350))
/gene="F3N23.6"
/note="Similar to entire sequence of downy mildew
/note="Similar to RPP5 [Arabidopsis thaliana]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Similar to N-terminal half of resistance protein RPP5 [Arabidopsis (gi 2109275)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="F3N23.5"
join(16543. .16961,17058. .17907)
/gene="F3N23.5"
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SSIEVLSSLRTLCLNKCKKLKSIEGLPLCLKSLYAHGCEILETVSLPLNHSVKHLDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MASSSSSPIWKYDVFLSFRGEDTRKNIVSHLHKQLYDKGVVTFK
DDKKLELGDSISEEISRAIQNSTYALVILSENYASSSWCLDELRWYMDLHLKNKIKVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Similar to downy mildew resistance protein /protein_id="AAD55633.1" /db_xref="GI:5903075"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein RPP5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HCFGLKRDEHLIAQFLNEGENEEESLGFAFFPGTEVPSYFDHIDKGKSLTIDLPQIWP
SPKLLGFDACVVIACERPFDIQFSPFSYDWDWGYERYFCLYLKPDFHSTDPSTEDEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                         7.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 8;
1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                   214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 116944;
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thaliana]
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                                              84762
                                                                                                                                                                                                                                 84642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-NOV-1996) USDA, ARS, Appalachian Fruit Research Station, 45 Wiltshire Road, Kearneysville, WV 25430, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 5033)
Bassett,C.L., Cohen,R.A., Nickerson,M.L. and Rajeevan,M.S.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Convolvulaceae;
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ITQSWNASDSTPCSWLGVECDRROFVDTILNISSYGISGEFGPEISHLKHIKKVVLSGN
GFFGSIPSOLGNCSLLEHIDLSSNSTTGNIDITIGALONLRHILSLFFNSLIGPFPESL
LSIPHLETVYFTGNGLNGSIESHIGNKSELTTILADDNQFSGPVPSSLGNITTIQELY
LNDNNLVGTLPVYFTGNGLNGSIESNIGNKSELTTILADDNQFSGPVPSSLGNITTIQELY
LNDNNLVGTLPVYELNULENLYYLDVRNNSLVGALFLDFVSCKQLDTISLSNNQFTGGL
PPGLGNCTSLREFGAFSCALSGPIPSCFGQLTKLDTLYLANGERGRIPPELGKCKSM
IDLQLQQNQLEGEIPGELGMLSQLQYLHLYTNNLSGEVPLSTWKIQSLQSLQLYQNNL
SGELDVDMTEIKQUVSLALYENHETGYIPQDLGANSSLEVLDLJRINNETGHIPPILCS
QKKLKRLLLGYNYLEGSVPSDLGGCSTLERLILEENNLRGGLPDFVEKQNLLFFDLSG
NKHTGPIPPSGLGNLKNVTALYLSSNSLSSSTPSGGLFSSGGIPSELFQNKKLLNL
LSNCHKLSELDASHILLNGSIPSTLGSLTLETTKLSLEENSFSGGIPSELFQNKKLLNL
QLGGNLLAGDIPPVGALQALRSLNLSSNKLNGQLPIDLGKKKMLEELDVSHNNLSGTL
RVLSTIQSTLTSINLFSGFVPPSLTKFLNSSPTSFSGNSTLTKOPSCHOPSTAR
RVLSTIQSTTTTILTTATUTGALTTTTATUTGALTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               681. .695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="young leaf" 237. .251
                                                                                                                                                                                                                                                                                                                                                         /product="receptor-like protein kinase"
/protein_id="AAB36558.1"
/db_xref="G1:1684913"
/translation="MKVAVNTFLLSLCSTSSIYAAFALNSDGAALLSLTRHWTPIPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1144. .4566
/gene="inrpk1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:35883"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Ipomoea nil"
/cultivar="Violet"
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/gene="inrpk1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCAATTCCTTCCCAGCTAGGCAATTGCAGTCTTCTTGAACACATAGATCTGTCCTCCAA
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               Submitted (15-JAN-2000) P. Street, Albany, CA 94710, 3 (bases 1 to 81513)
                                                                                                                                                                          1 (bases 1 to 81513)
Liu,S.X., Sakano,H., Yu,G., Lee,J.M., Lenz,C., Pham,P., Toriumi, Chin,C., Chiou,J., Choi,E., Chung,M., Gonzalez,A., Howng,B., Liu,A., Vaysberg,M., Altafi,H., Brooks,S., Buehler,E., Chao,Q., Conn,L., Conway,A.B., Hansen,H., Johnson-Hopson,C., Khan,S., Kim,C., Lam,B., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R., Federspiel,N.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Veridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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TRHNIAYGTAHGLAYLHEPCDPA IVHRDIKPMYILLDSDLEPHISDFGTAKLDQSAT
SIPSNTVQGTIGYMAPENAFTTVKSRESDVYSYGVVLLELITRKKALDPSFNGETDIV
GWVRSVMTQTGEIQKIVDPSLLDELIDSSVMEQVTEALSLALRCAEKEVDKRPTMRDV
VKQLTRWSIRSYSSSYRNKSK"
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L Submitted (09-FEB-2000) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
On Feb 11, 2000 this sequence version replaced g1:6693723.
The sequence is of BAC F1407 from Arabidopsis thaliana chromosome
1. The sequence does not represent the sequence of the entire
insert of this clone. It is shorter by 6954 bp because we submit only the unique sequence of the clone. However, in order to facilitate the joining of overlapping clones in the future for creation of larger contigs, we provide small overlaps (200 bp) between overlapping sumbitted clones. The 5' end of this sequence overlaps by 200 bp to the 3' end of the sequence of the clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTATTCTTTATCTTTACGAGAACTATTTAACTGGTGTCATTCCCCCGGAACTAGGCAACA 2645
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Arabidopsis thaliana ch
complete sequence.
AC011765.4 GI:6539234
Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Benoman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome I BAC FIM20 genomic Unpublished
                                                                                                                                                  Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                       thale cress.
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/clone="F14D7"
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/cultivar="Columbia"
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53.7%;
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Pred. No. 3.2e
0; Mismatches
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3.2e-10;
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                                                                   Barnstead, M.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rockville, MD 20850, USA
e-mail: xiln@tigr.org
BAC clone F1M20 is from Arabidopsis chromosome I and is near the
molecular marker mi425.
The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission Submitted (14-007-1999) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org 3 (bases 1 to 134402)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Dec 8, 1999 this sequence vo
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Medical Center Dr.
                                                                                               /.uure="exon predicted by xgrail, quality good_shadowexon" complement(1509. 1530)
/note="exon predicted by xgrail, quality marginal" complement(1901,c1655. 1777,1908. .2135,2258. .2581, 2679. .2963,3052. .>3429))
/gene="Fix20.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="exon predicted by xgrail,
complement(744. .1286)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="exon predicted by xgrail, complement(393. .453)
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marginal_shadowexon"
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complement(1356. .1475)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
/cultivar="Columbia"
/db_xref="taxon:3702"
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1271. .1354
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/map="m1425"
                                                                                       complement(<1655.
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                  /note="similar to p58 protein kinase GB:AAB59449 [Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'clone="F1M20"
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                  repeat_region
                                                                                                                                                                                                                                                                                                               /product-"putative type II intron maturase"
/product-"putative type II intron maturase"
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/db_xref-"gii639237"
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ELSGGVPDVASNYESIVABOKYREVILVESVALKVVDEAIRTVLEVYSPBTSKISHS
CRSGRGRASALKYINNISRSDMCFTLSLNKKLDVSVFENLLSVMEEKVEDSSLSILL
RSMTEARVLNLEFGGFPKGHGLPPEGVLSRVLANIYLDREFPERTSKISHSLGLDS
CRSGRGRASALKYINNISRSDMCFTLSLNKKLDVSVFENDEIYTSVGSPKVAD
LRSMTEARVLNLEFGGFPKGHGLPPEGVLASVLANIYLDREFPKTSVGFPKVAD
KTDEDSGSKLTSMFFRRQAGEDQLKSTTEDDVALFVLGCRENDEIYTSVGSPKVAD
LRSEAIGFLRNSLHLDITDETDPSDCEATSGLEVLGTLVRKNVERSPTVKAVHKLKEK
VRLFALQREEAWFLGTNRAGEDQLKSTTEDDVALFVLGCRENDEIYTSVGSPKVAD
LRSEAIGFLRNSLHLDITDETDPSDCEATSGLEVLGTLKVLRESSPTVKAVHKLKEK
VRLFALQREEAWFLGTNRAGEGEVAFTNAIGRRLYRGLITAKGYRRSNSMLILLD
INSEALIGESTANLEALLFCPGSHDRPVFFGDVVAFTNAIGRRLYRGLITAKGYRRSNSMLILLD
TAQIIDWSGLVRRWINTWYEGGSNEDELKALLDNGIRNSCLEFLAAKYRIHBNETEKR
LDLELSTIPSAEDIEDEIOHEKLDSPADDRDEHLTYGLSNGGLCLLSLARLVSESRPC
NCFVTGCSMAAPAVTLHAMERQKFPGWKTGFSVCIPSSLNGRRIGLCKQHLKDLYIG
QISLQAVDGAWR"
CCRLFTCRLYTOS
                                                                                                                            marginal,
8935. .9
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/note="exon predicted by xgrail, quality excellent"
complement(join(<4608..4760,4885..>4974))
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2679..2963,3052..3429))
/gene="flM20.1"
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/gene="F1M20.3"
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/note="exon predicted by complement(<5342. .>7603)
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/gene="FIM20.2"
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SVKFMAREILILRRLNHPNIIKLEGLITSKLSCNIQLVFEYMEHDLTGLLSSPDIKFT
TPQIKCYMKQLLSGLDHCHSRGVMHRDIKGSNLLLSNEGILKVADFGLANFSNSSGHK
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/translation="MGCYSSKQTVSVTPAIDHSGVFKDNENECSGSGRIVVEDPPRPT
/translation="MGCYSGSELGSESGRASDSLSFRLGNVSRYLEAEQVAAGWPAWL
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protein kinase domain"
9333. . 3000 M333 . . 3000 your marginal_shadowexon"
9421. .9528
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/gene="F1M20.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="G1:6539236"
/translation="MELADRAYGLLSSISLSIFTYYTFWYIILPEYDSDHFIHKYFL
PODYALLYPYFAGIALLSLISYPIGMYMLKSKKKKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative dolichyl-phosphate mannosyltransferase polypeptide 2"
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polypeptide 2 GB:450365 [Homo sapiens] (regulator of
dolichol phosphate-mannose synthesis: EMBO J 1998 Sep
1;17(17):4920-9)"
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HKRGTASSALVSQYTTKPFACDPSSLPIYPPSKEIDTKHRDEAARSVISFIT"
                                                                                                                                8771. . 8821
/note="exon predicted by xgrail,
marginal_shadowexon"
                                                                                                                                                                                                                                                                                             complement(7885.
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                                                                                                                                                                                                                                                         xgrail,
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                                                                                                                                                                                                                                                         quality marginal"
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Query Match
Best Local Similarity
Matches 171; Conserv
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                                                                                                                                                                          12283 CAGGAGAATCCCTCGAGAGATTGGCAACTGCACAAGCCTTTTGTGGTTTAACGTGGCAA 12342
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DVVCQWPGIICTPQRRRVTGINLTDSTISGPLFKNFSALTELTYLDLSRNTIEGEIPD

DLSRCHNIKHLALSHNILEGELSLPGLSNLEVLDLSLNRITGDISSFPLFCNSLVVA

NLSTNNFTGRIDDIFNGCRNLKYDDFSSNRFSGEVMTGFGRLVESVADNHLSGNISA

SMFRONCTLQMLDLSONAFGGEFPGOVSNCQNLNVLNLMGMKFTGNIPAEIGSISSK

GLYLGNNTFSRDIFNCTANLTINLYFLDLSRNKFGGDIQEIFGRFTQVKYLVLHANSYV

GGINSSNILKLPLKSRLDLGYNNFSGOLFTELSQIQSLKFLILAXNNFSGDIPOEYGN

MPGLQALDLSFNKLTGSIPASFGKLTSLLMMLANNSLSGEIPREIGNCTSLMFNVA

NNQLSGRFHPELTRMGSNPSFTFEVNRQNKDKILAGSEELAMKRWIPASISOM

ALLTKKSCRSLMDHVLKYGLLFPVCSAGSTVFTLKISAXLQLSGNKFSGEIPASISOM

DRLSTLHLGFNEFEGKLPPEIGQLPLAFINLTRNNFSGEIPQEIGNLKCLONLDLSFN

NFSGNPTSLNDLNELSKFNISYNPFISGAIFTYADILKATSNFSEERVVGRGGY

GGSNTRHDMTSSSGGSSPWLSGKIKVIRLDKSTFTYADILKATSNFSEERVVGRGGY

GTVYRQVLPDGGEVATVKLOREGELSKEFFAEKEFLDAAFGGWAHPHLVRLYGGGTUFBL

GTVYRQVLPDGGEVATVKLOREGESKEFFAEKEFTAAMFGDMAHPHLVRLYGGGTUFBC

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GTVYRQVLPDGGESTAAMFGDMAHPHLVRLYGGTUFBC

GTVYRQVLPDGGESTAAMFGDMAHPHLVRLYGGTUFBC

GTVYRQVLPDGGESTAAMFGDMAHPHLORTGESTUFBC

GTVYRQTAGGTUFBC

GTVRGTAAMFGDMAHPHLORTGESTAAMFGDMAHPHLVRLYGGTUFBC

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GB:AAC49810 (putative receptor protein kinase); contains
Pfam profiles: PF00560 Leucine Rich Repeat (17 repeats),
PF00069 Eukaryotic protein kinase domain"
10992. .14231
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/note-"exon predicted by xgrail, quality marginal"
10574. .10662
/note-"exon predicted by xgrail, quality good"
<10992. .>14231
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VKASNVLLDKHGNARVTDFGLARLLNVGDSHVSTVIAGTIGYVAPEYGQTWQATTRGD
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/protein_id="AAF15908.1"
/db_xref="G1:6539238"
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/gene="F1M20.4"
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N W09743427-A1.

P 13-MAY-1997; E02443.

R 14-MAY-1996; GE-010044.

A (NOVS ) NOVARTIS AG.

De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;

De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;

P P P SDB; W47022.

R P-PSDB; W47022.

T Production of apomictic seeds - useful in plant breeding

T Production of apomictic seeds - useful in plant breeding

T Production of apomictic seeds - useful in plant breeding

T Production of apomictic seeds - useful in plant breeding

T Production of apomictic seeds - useful in plant breeding

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T Production of apomictic seeds - useful in plant breeding

C SIRK LER (leucine-rich repeat) sequences.

C SERK LER (leucine-rich repeat) sequences.

C SERK LER (leucine-rich repeat) sequences.
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V06590;
03-AUG-1998 (first entry)
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST clone.
receptor kinase; apomixis; apomictic; seeds; product
plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
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Pred. No. 3.6e-287;
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360 360 300 240 240 180 180 120 120 60 Result No.

Score

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Database

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N W09743427-A1.

D 20-NOV-1997.

E 13-MAY-1997; E02443.

F 13-MAY-1996; GB-010044.

R (NOVS ) NOVARTIS AG.

A (NOVS ) NOVARTIS AG.

De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;

R WPI; 98-086529/08.

R P-PSDB; W47018.

R P-PSDB; W47018.

C Production of apomictic seeds - useful in plant breeding Production of apomictic seeds - useful in plant breeding Sclaim 28; Pages 71-73; 123pp; English.

C The sequence is that of an EST clone showing high homology to SERK LRR (leucine-rich repeat) sequences.
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V06586;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST clreceptor kinase; apomixis; apomictic; seeds; pr plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
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ATGAAGA :gtaaaat	ctttato	GACAATO GAGATTO CGAGATTO CGAGATTO CGAGATTO CACAACTG	Ittgaag TTGAAG TTGAAG 	CTAGAGCTCTACAAAAA CTAGAGCTCTACAAAAA AAtotcatcagcttgga	ctggttc CTGGTTC AAACCTC	Ctttgattcacct	aaaatt aaaaTTTTCC tcacatggcg 	; 3 Leng
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DE Arabidopsis thaliana SERK LRR homologous ES;
W receptor kinase; apomixis; apomictic; seeds;
W plant breeding; leucine-rich repeat; ss.
S Arabidopsis thaliana
I Key
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20-NOV-1997.

13-MAY-1997; E02443.

14-MAY-1996; GB-010044.

(NOVS ) NOVARTIS AG.

10- Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;

R WPI; 98-086529/08.

R P-FSDB; W47019.

Production of apomictic seeds - useful in plant breed production of apomictic seeds - useful in plant breed of the sequence is that of an EST clone showing high hom SERK LRR (leucine-rich repeat) sequences.

Sequence 981 BP; 286 A; 236 C; 180 G; 2
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Pred. No. 1.7e-225;
0; Mismatches 32;
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V06588;
V06588;
T 03-AUG-1998 (first entry)
T non-Event thaliana SERK LRR homologous ES'
KW receptor kinase; apomixis; apomictic; seeds
plant breeding; leucine-rich repeat; ss.
plant consist thaliana.
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Best Local S
Matches 775
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20-NOV-1997.

13-MAY-1997; BC2443.

14-MAY-1996; BB-010044.

R (AOVS) NOVARTIS AG.

De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;

R P-PSDB; W47020.

R P-PSDB; W47020.

T Production of apomictic seeds - useful in plant breeding Claim 28; Pages 79-80; 123pp; English.

C The sequence 1s that of an EST clone showing high homology to SERK LRR (leucine-rich repeat) sequences.

Sequence 788 BP; 234 A; 191 C; 156 G; 207 T;
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20-NOV-1997.

13-MAY-1997; E02443.

14-MAY-1996; GB-010044.

(NOVS ) NOVARTIS AG.

De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;

WPI; 98-086529/08.

P-SSDB; W47021.

Production of apomictic seeds - useful in plant breed Claim 28; Pages 83-64; 123pp; English.

The sequence is that of an EST clone showing high hom SERK LRR (leucine-rich repeat) sequences.

Sequence 894 BP; 270 A; 163 C; 176 G;
                                                                                                                              V06589 standard; cDNA to mRNA; 894 BP.
V06589;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologou
receptor kinase; apomixis; apomictic; s
plant breeding; leucine-rich repeat; ss
Arabidopsis thaliana.
Key
Location/Qualifiers
CDS
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Best Local S
Matches 538
                   V06591 standard; cDNA to mRNA; 2089 BI
V06591;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK gene.
receptor kinase; apomixis; apomictic;
plant breeding, ds.
Arabidopsis thaliana.
Key
Location/Qualifiers
CDS
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Similarity 72.8%;
38; Conservative
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        SERK
                                               apomictic;
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Pred. No. 2e-91;
0; Mismatches 1
                                                seeds;
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The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with seed and forage quality and maturity.

Sequence 2089 BP; 568 A; 419 C; 503 G; 599 T;
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De Vries SC, Hecht VFG,
WPI; 98-086529/08.
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                               ccttttgctcacattcctttacagaactttgagaacaac 702
                                                                                          agcettaaagttgttgatgteteaageaatgatttgtgtggaacaateeeaacaaaegga
                                                                                                                                      CTCCGGCTTAACAACAACAGTCTCACTGGGTCAATTCCTATGTCACTGACCAATATTACT
                                                                                                                                                            TTAAACAGCTTCTCCGGTCCTATTCCGGAATCATTGGGGAAAGCTTTCAAAGCTGAGATTT
                                                                                                                                                                                                                                                                             ACTGGCCCGATTCCTAGTAATCTTGGAAATCTGACAAACTTAGTGAGTTTGGATCTTTAC
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                                                                  ACCCTTCAAGTGTTAGATCTATCAAATAACAGACTCTCTGGTTCAGTTCCTGACAATGGC
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GB-010044.
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Pred. No. 1.1e-49;
0; Mismatches 192;
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The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed appropagated hybrids and could shorten and simplify the breeding progens that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with seed and forage quality and maturity.

Sequence 1814 BP; 530 A; 354 C; 415 G; 515 T;
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14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, $
WPI; 98-086529/08.
P-PSDB; W47013.
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03-AUG-1998 (first entry)
Daucus carota SERK gene.
receptor kinase; apomixis; apomictic; seeds; production; embryos;
plant breeding; ss.
paucus carota.
Location/Qualifiers
Key
94. 1755
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CTCATTTTCTTTGTTTACACCTATCAGTTTTGCCAATAATTTGAATTTATGTGGACCCGT
                      accttttgctcacattcctttacagaactttgagaacaacccgaggttggagggaccgga
                                                                                            CTTGCGTCTCAACAACAACAGCCTCTCTGGTCCAATTCCAATGTCACTGACTAATATTAC
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                                                                     AACTOTTCAAGTCCTGGATTTATCAAACAATCGGCTATCAGGACCAGTACCGGATAATGG
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Pred. No. 1.8e-19;
0; Mismatches 161
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Best Local Similarity
Matches 169; Conserv
X23526;
X23526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding plant morphogenesis regulatory protein - useful to yield plants with short stems or altered inflorescence Claim 1; Pages 6-10; 17pp; Japanese.

The present sequence encodes an Arabidopsis thaliana plant morphogenesis regulatory protein (MRP), which can be used to yie a plant with, e.g. short stems or altered inflorescence. The MRP acts on a plant at a specific site for a specific period, and can therefore be used to regulate extraneous gene expression in a plant. The MRP; cDNA or genomic DNA can be used to transform a plant to increase its MRP expression, and therefore control the form (particularly stem length) of the plant.

Sequence 3176 BP; 927 A; 654 C; 659 G; 936 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-AUG-1995; 216187.
24-AUG-1995; JF-216187.
24-AUG-1995; JF-216187.
24-AUG-1995; JF-216187.
AITSUI GYOSAI SHOKUBUTSU
(CHIK-) ZH CHIKYU KANKYO SANGYO G
WPI; 97-206629/19.
P-PSDB; W13408.
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10-JUN-1997
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                                                                                  GCAACAATATCAAAGGTCCAATCCC
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/note= "plant morphogenesis regulatory
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Pred. No. 1.5e-11;
0; Mismatches 156;
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659 G;
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O. longistaminta Xa21 gene f.
Xa21; receptor kinase-like p.
plant disease resistance; ca.
Oryza longistaminata.
W09909151-A2.
25-FEB-1999.
17-JUL-1998. U14841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 case to be used for tomato rice or tomato 5940 BP;
                  11-MAY-1995; G01075.

11-MAY-1994; GB-009394.

23-DEC-1994; WO-G02812.

31-MAR-1995; GB-006658.

07-APR-1995; GB-007232.

(GATS-) GATSBY CHARITABLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New RRK polynucleotides and nucleic acid
generating transgenic plants resistant to
Glaim 1; page 52-53; 67pp; English.
This invention describes a method for con
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WPI; 99-204431/17.
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(REGC ) UNIV CALIFORNIA.
Hulbert SH, Richter T, Ronald PC,
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                                                                                                                                                                                                                       Partial tomato pathogen resistance gene Cf-2.2 Pathogen resisitant; Cf-2.2; tomato; C.fulvum; leaf mould; variegation; ss.
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       Hammond-Kosack
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  CHARITABLE KE, Jones
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e protein; multicassava; maize;
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igene family; RRK; rice;
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Matches
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Claim 9; Page 85-87; 131pp; English.

T06307 is a tomato pathogen resistance gene Cf-2.2 partial cDNA clone. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagules of plants) containing such constructs. Cf-2.2 imparts resistance to the disease caused by the leaf mould fungal pathogen cladosporium fulvum. C.fulvum contains avirulence (Avr) genes that confer recognition by plants containing Cf-genes, leading to the activation of host defence mechanisms to attack the disease.

Sequence 3573 BP; 1032 A; 654 C; 664 G; 1223 T;
23-NOV-1995;
11-MAY-1995;
11-MAY-1994;
11-MAY-1994;
23-DEC-1994;
31-MAR-1995;
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P-PSDB; R85299.
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1746. .5011
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1677. .5014
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Pred. No. 2e-10;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; fungal;
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"GATSBY CHARITABLE FC

"Ammond-Kosack KE, Jones P*

R WPI; 96-010949/01.

P-P5DB; R85298.

Increasing p'

"Ja"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Increasing plant pathogen resistance by induction of variegation may lead to acquired resistance to a broad range of pathogens.

Claim 9; Page 80-83; 131pp; English.

T06306 is the tomato pathogen resistance gene Cf-2.1. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagules of plants) containing such constructs. Cf-2.1 imparts resistance to the disease caused by the leaf mould fungal pathogen Cladosporium fulrum.

C. fulrum contains avirulence (Avr) genes that confer recognition by plants containing Cf-genes, leading to the activation of host defence mechanisms to attack the disease.

Sequence 6471 BP; 2073 A; 1106 C; 1122 G; 2170 T;
                                                                                                                                                                                                                  plant
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                                                                                                                                                                                                                            03-AUG-1998 (first entry)
Arabidopsis thaliana SERK gene.
receptor kinase; apomixis; apomictic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3471 AACAACTTGTCTATGTTGTATCTTTACAATAATCAGCTTTCTGGCTCTATTCCTGAAGAA
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          intron
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                                                                                                                                                                                                                                                                                                                 12
                                                                                                                                                                                                                                                                                                                                                          GTTTTGTCGATGTCATCTAATAGTTTCAGTGGAGAGCTCCCTTCA
                                                                                                                                                                                                                                                                                                                                                                         gttgttgatgtctcaagcaatgatttgtgtgtggaacaatcccaaca
                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCATTGGGGAAATTCCTTCATCTGTGTGCAATTTGACATCACTGGAAGTGTTGTATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cttacagggatagttcccacttctttgggaaaattgaagtctctggtctttttacggctt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ataccttccgaacttggaaatctgaagaatctcatcagcttggatctgtacaacaacaat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAGGTTACTTGAGTTCTTACTTATCTATCTTTGGGTAATAACTCTCTTAATGGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cttgggaagcttgaacatttacagtatctagagctctacaaaaacaaccatccaaggaact
                                                                                                                                                                                                                                                                                                                                                                                                               CCGAGAAACAATTTGAAGGGAAAAGTTCCGCAATGTTTGGGTAATATCAGTAACCTTCAG
                                                                                                                                                                                                                   breeding; ds.
                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                    thaliana
                       4124. .4211
/*tag= d
/number= 3
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                                                                                         3851. .3979
                                                                                                                                                                                                                                                                                     DNA; 4081
                                                                                                      /number=
                                                                                                                                                                                       ocation/Qualifiers
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Pred. No. 2.
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                                                                                                                                                                                                                                seeds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
.6e-10;
                                                                                                                                                                                                                                production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6471;
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/number-4430. .45

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                          plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant to reeding programs. Controllable and reproducible apomixis provides commany advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed apomictic plant and could shorten and simplify the breeding propagated hybrids and could shorten and simplify the breeding process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with seed and forage quality and maturity.

Seed and forage quality and maturity.

Sequence 4081 BP; 1120 A; 770 C; 785 G; 1406 T;
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Production of apomictic seeds - useful in plant breeding Claim 26; Pages 64-67; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing
                                                                                                                                                                                                                                                                                       1794
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              03-AUG-1998 (first entry)
Daucus carota SERK gene.
receptor kinase; apomixis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NOVS ) NOVARTIS AG
                                                                            V06570 standard; DNA; 6695
                                                                                                                                                                                 ccgcgtcactcgtgtgga 332
                                                                                                                                                                                                                                                                                                        aggagatgctctttacgctcttcgccggagtttaacagatccggaccatgttctccagag
                                                                                                                                                           CAGTGTCATAAGAGTGTA 1931
                                                                                                                                                                                                                                         ctgggatccaactcttgttaatccttgtacctggttccatgtcacctgtaaccaagacaa 314
                                                                                                                                                                                                                                                                                       AGGTGATGCTTTGCATACTTTGAGGGTTACTCTAGTTGATCCAAACAATGTCTTGCAGAG 1853
                                                                                                                                                                                                                        CTGGGATCCTACGCTAGTGAATCCTTGCACATGGTTCCATGTCACTTGCAACAACGAGAA 191:
 breeding; ds
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GB-010044.
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              apomixis; apomictic; seeds; production; embryos;
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Pred. No. 3.2e
0; Mismatches
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.2e-10;
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aggagatgctctttacgctcttcgccggagttttaacagatccggaccatgttctccagag

l Similarity 96; Conserv

Conservative

42;

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Gaps

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1015

ctgggatccaactcttgttaatccttgtacctggttccatgtcacctgtaaccaagacaa 314 AGGCGATGCATTACACAACTTACGAACTAGCTTGCAAGATCCCAACAATGTCCTGCAGAG

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Production of apomictic seeds - useful in plant breeding production of apomictic seeds - useful in plant breeding scalaim 21; Pages 40-46; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing the transformed material into plants or carpel-containing that parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides commany advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the case that sexual plants are available as crosses with the programs of the case that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with specific stabil traits for such characteristics as height, seed and forage quality and maturity.

Sequence 6695 BP; 1844 A; 1182 C; 1243 G; 2422 T;
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14-MAY-1996;
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De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ, WPI; 98-086529/08.
P-PSDB; W47013.
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5295. 5803
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3851. .3979
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            6.7%;
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; Score 70.8; D
; Pred. No. 3.9e
0; Mismatches
               DB 1;
i.9e-10;
                            Length 6695;
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RESULT
V14518
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CC This sequence is an example of the polynucleotide of the invention, and CC is able to confer pathogen resistance on a plant. It is one of two tomato CC F-5 gene variants, which offer resistance against the pathogen CC the gene into plant cells and regenerating plants from the cells; CC asswally or sexually produced offspring can also be subsequently CC produced. Expression of the gene in plant cells can confer pathogen CC resistance on a plant e.g. to tomato leaf mould (C. fulvum) in tomatoes. CC Oligonucleotides with sequences complementary to the gene or fragments CC of it, are useful in anti-sense techniques to reduce gene expression. The CC identify other genes/fragments conferring pathogen resistance on plants cc.g. phytophthora resistance in potatoes. Homologies between Cf-5 and CC cf-9 may be used to identify further resistance genes of this class. 50 Sequence 3979 Bp; 1217 A; 717 C; 698 G; 1347 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
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                                                                                               2124
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09-MAY-1996; GB-009681.

(INNE-) INNES CENT INNOVATIONS LTD JOHN.
DIXON MS, Hatzixanthis K, Jones DA, Jone
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Tomato; CF-5 pathogen resistance gene; Cladosporium fulvum-5;
tomato leaf mould; Phytophthora resistance; ss.
Lycopersicon pimpinellifolium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1944 AACAACTTGTTTATGTTGTATCTTTACAATAATCAGCTTTCTGGCTCTATTCCTGAAGAA 2003
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                                                                                                                           cttacagggatagttcccacttctttgggaaaattgaagtctctggtctttttacggctt 552
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Pred. No. 3
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is an example of the polynucleotide of the invention, and is able to confer pathogen resistance on a plant. It is one of two tomate CF-5 gene variants, which offer resistance against the pathogen cladosporium fulvum-5. Transgenic plants can be produced by incorporating the gene into plant cells and regenerating plants from the cells; asexually or sexually produced offspring can also be subsequently produced. Expression of the gene in plant cells can confer pathogen resistance on a plant e.g. to tomato leaf mould (C. fulvum) in tomatoes. Oligonucleotides with sequences complementary to the gene expression. The nucleic acids/polynucleotides are useful as hybridisation probes to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09743429-A1.
20-NOV-1997.
08-MAY-1997; (
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Tomato; CF-5 pathogen resistance gene; Cladd tomato leaf mould; Phytophthora resistance; Lycopersicon pimpinellifolium.

Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identify other genes/fragments conferring pathogen resistance on plants e.g. Phytophthora resistance in potatoes. Homologies between Cf-5 and Cf-9 may be used to identify further resistance genes of this class. Sequence 3979 BP; 1218 A; 716 C; 698 G; 1347 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tomato gene Cf-5, confers resistance to Cladosporium for production of transgenic plants resistant to path tomato leaf mould C. fulvum in tomatoes Claim 6; Fig 1b; 75pp; English.
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V14519;
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09-MAY-1996; GB-009681
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AGTGATAACGATCTCATTGGGGAAATTCCTTCATTTGTGTGCAATTTGACATCACTGGAA
                                                       ATAGGTTACCTGAGTTCTCTTACTGAACTATTTTTGGGTAATAACTCTCTTAATGGCTCT
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                                                                                                                    CTTTCTGGCTCTATTCCTGCTTCATTTGGCAATATGAGAAATCTGCAAACTCTGTTTCTC
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                                                                                                                                                                                                                                   ATTCCTGCTTCATTGGGGGAATCTAAACAACTTGTCTAGGTTGTATCTTTACAATAATCAG
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ilarity 50.4%;
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Pred. No. 3.6e-10;
0; Mismatches 169
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; Cladosporium
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